

This is a AL-2-long (AL-21) protein. The AL-2 is a novel Eph-related tyrosine kinase receptor ligand. AL-2 can be administered to patients in whom the nervous system has been damaged by trauma, surgery, stroke, ischemia, infection, metabolic disease, nutritional deficiency, malignancy, or toxic agents, to promote the survival or growth of neurons. They can be used to treat motoneuron disorders such as amyotrophic lateral sclerosis (Lou Gehrig's disease), Bell's palsy, and various conditions involving spinal muscular atrophy, or paralysis. AL-2 can be used to treat human neurodegenerative disorders, such as Alzheimer's disease, Parkinson's disease, epilepsy, demyelinating diseases such as multiple sclerosis, Huntington's chorea, Down's syndrome, nerve deafness, Menier's disease, and other disorders of the cerebellum. AL-2 can be used as cognitive enhancer, to enhance learning particularly in dementias or trauma, since they can promote axonal outgrowth and synaptic plasticity, particularly of hippocampal neurons that express AL-2 binding Eph-family receptors and cortical neurons that express AL-2. AL-2 can also be used for wound healing, i.e. accelerating neovascularisation of, e.g. burns and ulcers. The encoding nucleic acids are useful in preparing antibodies that specifically bind to the AL-2 protein. The antibodies and the AL-2 antagonists are useful in diagnosing and treating various neuronal disorders. AL-2 antagonists can be used for modulating angiogenesis. They can also be used for the treatment of tumours, acute myeloid leukaemia (AML), chronic myeloid leukaemia (CML), myelodysplastic syndrome (MDS), diabetic retinopathy, neovascular glaucoma, psoriasis and rheumatoid arthritis

Sequence 455 AA;

Query Match 100.0%; Score 2450; DB 2; Length 455;

Best Local Similarity 100.0%; Pred. No. 3.6e-197; Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MGPPHSGPGVAVGALLLGLVGLVGLSLPEVYNNSSANKRFQAEQGYLYLPQIGRDL 60
DB 1 MGPPHSGPGVAVGALLLGLVGLVGLSLPEVYNNSSANKRFQAEQGYLYLPQIGRDL 60
QY 61 LCPRARPPGPHSSPNVEFYKLYLVGAQGRCEAPPAPNLLITCDRPDLDRFTIKFOEY 120
DB 61 LCPRARPPGPHSSPNVEFYKLYLVGAQGRCEAPPAPNLLITCDRPDLDRFTIKFOEY 120
QY 121 SPNLWGHERRSHHDYIITSDTRREGSLQGVCLTRGMKYLAVGQSPGGAVPKRP 180
DB 121 SPNLWGHERRSHHDYIITSDTRREGSLQGVCLTRGMKYLAVGQSPGGAVPKRP 180
QY 181 VSEMERDERGAHAHSLPEKENVLPDPTSNATSRGAEGPLPPSPMDVAGAGLALL 240
DB 181 VSEMERDERGAHAHSLPEKENVLPDPTSNATSRGAEGPLPPSPMDVAGAGLALL 240
QY 241 GVAAGAGAACWRRRRRAKPEESRRHFGSGFGRGSLGLGGGGMGPPEAEPEGLALRG 300
DB 241 GVAAGAGAACWRRRRRAKPEESRRHFGSGFGRGSLGLGGGGMGPPEAEPEGLALRG 300
QY 301 GAADPFCHYEKVSQDYGHPVYIVDDGPQSPNYYTISVLEPPIHTTQLPFMRSK 360
DB 301 GAADPFCHYEKVSQDYGHPVYIVDDGPQSPNYYTISVLEPPIHTTQLPFMRSK 360
QY 361 CSRVTFFLPVQVYITSTCRMTSFTTINPMSQACRAQMGERRIMCFMGRIITGALF 420
DB 361 CSRVTFFLPVQVYITSTCRMTSFTTINPMSQACRAQMGERRIMCFMGRIITGALF 420
QY 421 VLVLLILLGLRLNHQTLLRQASVEAAGQHPL 455
DB 421 VLVLLILLGLRLNHQTLLRQASVEAAGQHPL 455

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RESULT 2
AAW31544
ID AAW31544 standard; protein; 340 AA.

AAW31544;

14-APR-1998 (first entry)

XX

DE Human cytokine Lerk-8.

XX Lerk-8; cytokine; human; hek; elk; receptor tyrosine kinase; ligand;

KW neurodegenerative disease; wound healing; neovascularisation; diagnosis;

XX therapy.

OS Homo sapiens.

FX Key Location/Qualifiers

FT Peptide 1..27 /label= Sig_peptide

FT Protein 28..340 /label= Mat_protein

FT Domain 28..224 /note= "extracellular domain"

FT Modified-site 210..212 /note= "N-glycosylated"

FT Domain 225..251 /note= "transmembrane domain"

FT Domain 252..340 /note= "cytoplasmic domain"

FT Misc-difference 325 /note= "residue 325 is Leu in Lerk-8 variant"

PN WO9736919-A2.

PD 09-OCT-1997.

XX 19-MAR-1997; 97WO-US004533.

XX 21-MAR-1996; 96US-00621146.

XX (IMMUNEX CORP.

PI Corrected DP;

DR WPI, 1997-503043/46.

XX N-PSDB; AAT89519.

PT New isolated cytokine, Lerk-8 - binds to the hek and elk receptor

PS tyrosine kinases, used to develop products for diagnosis and therapy.

XX Claim 3; Page 32-33; 37pp; English.

CC This protein sequence comprises a novel human cytokine designated Lerk-8.

CC The amino acid sequence was deduced from a human foetal brain cDNA clone

CC (see AAT89519). Lerk-8 binds to the cell surface receptors hek and elk,

CC which are members of the eph/elk family of receptor tyrosine kinases.

CC Lerk-8 polypeptides, especially soluble polypeptides comprising amino

CC acid residues -27 to 142-197 of the full-length protein, can be purified

CC in transformed host cells. These polypeptides can be used to purify hek

CC or elk proteins, and to purify or identify cells that express hek or elk

CC on the surface. Such cells can be used in various in vitro studies or in

CC vivo procedures, e.g. neural cells expressing elk can be administered to

CC a mammal afflicted with a neurodegenerative disorder. The Lerk-8

CC polypeptides can also be used to deliver diagnostic or therapeutic agents

CC to these cells (e.g. leukaemia cells). The Lerk-8 DNA and polypeptides

CC can also be used to treat disorders mediated by defective or

CC insufficient amounts of Lerk-8; to treat disorders such as injury to

CC neural tissue or neurologic disease; to promote angiogenesis; and for

CC wound healing or stimulating neovascularisation of grafted tissues

XX Sequence 340 AA;

Query Match 75.1%; Score 1841; DB 2; Length 340;

Best Local Similarity 100.0%; Pred. No. 4.1e-146; Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MGPPHSGPGVAVGALLLGLVGLVGLSLPEVYNNSSANKRFQAEQGYLYLPQIGRDL 60
DB 1 MGPPHSGPGVAVGALLLGLVGLVGLSLPEVYNNSSANKRFQAEQGYLYLPQIGRDL 60
QY 61 LCPRARPPGPHSSPNVEFYKLYLVGAQGRCEAPPAPNLLITCDRPDLDRFTIKFOEY 120

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Db      |||||
Qy      61 LCPRARPPGPHSSPNVEFYKLYLVGAQGRCEAPPAPMLLTCDRDLFTTIKFOEY 120
Db      121 SPNLNGHERSHHDYIIITSDGTRBGLSLGGCVLTGTMVTLRVGSPRGANPRP 180
Qy      121 SPNLNGHERSHHDYIIITSDGTRBGLSLGGCVLTGTMVTLRVGSPRGANPRP 180
Db      181 VSEMERDRGAHSLPEKENTLPGDPTSNATSRGAEGLPPSPMPAVAGAAGLALLLL 240
Qy      181 VSEMERDRGAHSLPEKENTLPGDPTSNATSRGAEGLPPSPMPAVAGAAGLALLLL 240
Db      181 VSEMERDRGAHSLPEKENTLPGDPTSNATSRGAEGLPPSPMPAVAGAAGLALLLL 240
Qy      241 GVAAGAGAMCWRRRRAKPSRRHPGSGFRGSGSLGLGGGGMGPREAPGELGIALRGG 300
Db      241 GVAAGAGAMCWRRRRAKPSRRHPGSGFRGSGSLGLGGGGMGPREAPGELGIALRGG 300
Qy      301 GAADPPFCPHYEKVSGDYGHPIYIVODGPPQSPPNIIY 338
Db      301 GAADPPFCPHYEKVSGDYGHPIYIVODGPPQSPPNIIY 338

RESULT 3
AAW33699
ID      AAW33699 standard; protein, 340 AA.
AC      AAW33699;
XX      30-APR-1998 (first entry)
XX      DE
XX      AL-2-short (AL-2s) protein.
XX      AL-2s; AL-2-short; human; treatment; neurological disorder; tumour;
XX      rheumatoid arthritis; wound healing; paralysis; angiogenesis; leukaemia;
XX      psoriasis; Alzheimer's disease; epilepsy.
XX      Homo sapiens.
XX      OS
XX      FH
XX      FH Peptide 1..26
XX      FT /note="signal peptide"
XX      FT Protein 27..340
XX      FT /note="mature protein"
XX      FT Domain 27..219
XX      FT /note="extracellular domain"
XX      FT Domain 220..245
XX      FT /note="hydrophobic transmembrane domain"
XX      PN
XX      WO9740153-A1.
XX      PD 30-OCT-1997.
XX      PF 17-APR-1997; 97WO-US006345.
XX      PR 19-APR-1996; 96US-00635130.
XX      PA (GETH ) GENENTECH INC.
XX      PI Caras IW;
XX      DR WPI, 1997-535837/49.
XX      DR N-PSDB; AAV06355.
XX      PT Human AL-2 neurotrophic factor and related DNA - used to develop products
XX      for, e.g. treating neurologic disorders, angiogenesis disorders, tumours
XX      or rheumatoid arthritis or for wound healing.
XX      PS Claim 20; Fig 2A-B; 86pp; English.
XX      CC This is a AL-2-short (AL-2s) protein. The AL-2 is a novel Eph-related
XX      tyrosine kinase receptor ligand. AL-2 can be administered to patients in
XX      whom the nervous system has been damaged by trauma, surgery, stroke,
XX      ischaemia, infection, metabolic disease, nutritional deficiency,
XX      malignancy, or toxic agents, to promote the survival or growth of
XX      neurons. They can be used to treat motoneuron disorders such as

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CC      amyotrophic lateral sclerosis (Lou Gehrig's disease), Bell's palsy, and
CC      various conditions involving spinal muscular atrophy, or paralysia. AL-2
CC      can be used to treat human neurodegenerative disorders, such as
CC      Alzheimer's disease, Parkinson's disease, epilepsy, demyelinating
CC      diseases such as multiple sclerosis, Huntington's chorea, Down's syndrome,
CC      nerve deafness, Menier's disease, and other disorders of the cerebellum.
CC      AL-2 can be used as cognitive enhancer, to enhance learning particularly
CC      in dementias or trauma, since they can promote axonal outgrowth and
CC      synaptic plasticity, particularly of hippocampal neurons that express AL-
CC      2 binding Eph-family receptors and cortical neurons that express AL-2. AL-
CC      2 can also be used for wound healing, i.e. accelerating
CC      neovascularisation of, e.g. burns and ulcers. The encoding nucleic acids
CC      are useful in preparing antibodies that specifically bind to the AL-2
CC      protein. The antibodies and the AL-2 antagonists are useful in diagnosing
CC      and treating various neuronal disorders. AL-2 antagonists can be used for
CC      modulating angiogenesis. They can also be used for the treatment of
CC      tumours, acute myeloid leukaemia (AML), chronic myeloid leukaemia (CML),
CC      myelodysplastic syndrome (MDS), diabetic retinopathy, neovascular
CC      glaucoma, psoriasis and rheumatoid arthritis
XX      CC
XX      SQ Sequence 340 AA;
XX      Query Match 75.1%; Score 1841; DB 2; Length 340;
XX      Best Local Similarity 100.0%; Pred. No. 4.1e-146;
XX      Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1 MGPPHSGGCVAVGALLLGLVGLVSGLSLEPVYNNANAKRFOEGGYLYPOIGRLDL 60
Db      1 MGPPHSGGCVAVGALLLGLVGLVSGLSLEPVYNNANAKRFOEGGYLYPOIGRLDL 60
Qy      61 LCPRARPPGPHSSPNVEFYKLYLVGAQGRCEAPPAPMLLTCDRDLFTTIKFOEY 120
Db      61 LCPRARPPGPHSSPNVEFYKLYLVGAQGRCEAPPAPMLLTCDRDLFTTIKFOEY 120
Qy      121 SPNLNGHERSHHDYIIITSDGTRBGLSLGGCVLTGTMVTLRVGSPRGANPRP 180
Db      121 SPNLNGHERSHHDYIIITSDGTRBGLSLGGCVLTGTMVTLRVGSPRGANPRP 180
Qy      181 VSEMERDRGAHSLPEKENTLPGDPTSNATSRGAEGLPPSPMPAVAGAAGLALLLL 240
Db      181 VSEMERDRGAHSLPEKENTLPGDPTSNATSRGAEGLPPSPMPAVAGAAGLALLLL 240
Qy      241 GVAAGAGAMCWRRRRAKPSRRHPGSGFRGSGSLGLGGGGMGPREAPGELGIALRGG 300
Db      241 GVAAGAGAMCWRRRRAKPSRRHPGSGFRGSGSLGLGGGGMGPREAPGELGIALRGG 300
Qy      301 GAADPPFCPHYEKVSGDYGHPIYIVODGPPQSPPNIIY 338
Db      301 GAADPPFCPHYEKVSGDYGHPIYIVODGPPQSPPNIIY 338

RESULT 4
AAW10637
ID      AAW10637 standard; protein, 340 AA.
AC      AAW10637;
XX      23-JUN-1997 (first entry)
XX      DE
XX      NLERK2 ligand for eph-related kinase.
XX      DE
XX      LERK, ligand for eph-related kinase; ERK; NLERK2;
XX      KW receptor protein tyrosine kinase; cell proliferation;
XX      KW cell differentiation; cell survival; nerve cell.
XX      OS
XX      FH
XX      FH Key Location/Qualifiers
XX      FT Peptide 1..29
XX      FT Protein /label= Sig_peptide
XX      FT /label= Mat_protein
XX      FT Modified-site 210

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FT FT /label= N-glycosylation_site
FT FT 227..251
FT FT /label= Transmembrane_domain
PN WO9704091-A1.
XX
XX
XX 06-FEB-1997.
PD
XX
XX 19-JUL-1996; 96WO-AU000460.
XX PF
XX PR 20-JUL-1995; 95AU-00004263.
XX PR 27-NOV-1995; 95AU-00006847.
XX PR 22-DEC-1995; 95AU-00007299.
XX PR 05-FEB-1996; 96AU-00007890.
XX
XX (AMRAD-) AMRAD OPERATIONS PTY LTD.
XX
XX Nicola NA;
PI
XX WPI, 1997-132632/12.
XX DR N-PSDB; AAT60966.
XX
XX Nucleic acid mol. encoding ligand for eph-related kinase - useful for
PT treatment of, pret. neuronal, cells to increase survival, proliferation
PT and differentiation.
XX
XX Claim 16; Page 37-39; 71pp; English.
XX
XX A novel human ligand for eph-related kinase (LERK) is designated NLERK2
CC (AA010637). It is encoded by a cDNA clone (AAT60966) obt'd. from a human
CC foetal brain cDNA library. The novel receptor ligand can be expressed in
CC transformed host cells and used in methods for regulating the
CC development, maintenance or regeneration of different cells (e.g.
CC neurons) and tissues in vivo and in vitro. Soluble NLERK2 peptides can be
CC used to treat injury, disease or abnormality in the nervous system, and
CC membrane-bound NLERK2 to modulate proliferation, different or survival
CC e.g. in grafting procedures or transplantation. NLERK2 can also be used
CC to raise antibodies for use in immunotherapy, and to detect anti-NLERK2
CC antibodies that may occur in some autoimmune diseases
XX
XX Sequence 340 AA;
SQ
Query Match 75.1%; Score 1841; DB 2; Length 340;
Best Local Similarity 100.0%; Pred. No. 4.1e-146;
Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGPPHSGPGGVAVGALLLGLVGLVSGLSLEPYVYNSANKRFOAEGGYLYPOIGDRLDL 60
DB 1 MGPPHSGPGGVAVGALLLGLVGLVSGLSLEPYVYNSANKRFOAEGGYLYPOIGDRLDL 60
QY 61 LCPRARPPGPHSSPNVEFYKYLIVGGAQGRCEAPPAPNLLITCDRDLRFTIKFOEY 120
DB 61 LCPRARPPGPHSSPNVEFYKYLIVGGAQGRCEAPPAPNLLITCDRDLRFTIKFOEY 120
QY 121 SPNLWGHFRSHHDYIITATSDGTREGLESLOGGVCLTGMKYLIRVGQSPRGAVPRKP 180
DB 121 SPNLWGHFRSHHDYIITATSDGTREGLESLOGGVCLTGMKYLIRVGQSPRGAVPRKP 180
QY 181 VSEMPERERGAHSLPEKENVLPDPTSNATSRGEGGLPPSPMAVAVGAAGLALLL 240
DB 181 VSEMPERERGAHSLPEKENVLPDPTSNATSRGEGGLPPSPMAVAVGAAGLALLL 240
QY 241 GVAAGAGAACMRRARRKPSSESRHPGGSFGRGSLGLGSGGGMPPREAPGELGILRGG 300
DB 241 GVAAGAGAACMRRARRKPSSESRHPGGSFGRGSLGLGSGGGMPPREAPGELGILRGG 300
QY 301 GAADPPFCPHYEKVSGDYGHPIYIVDGPQSPPNITY 338
DB 301 GAADPPFCPHYEKVSGDYGHPIYIVDGPQSPPNITY 338
RESULTS 5
ABU07845
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ID ABU07845 standard; protein; 340 AA.
XX
XX AC ABU07845;
XX
XX 10-MAY-2003 (first entry)
XX
XX DE Human ephrin-B3 ligand.
XX
XX KW Cytostatic; vasodilator; antiinflammatory; cardiant; gene therapy;
KW ligand-receptor binding modulator; ephrin ligand; angiogenesis;
KW lymphangiogenesis; aberrant Ephrin-Tie biology; cell growth disorder;
KW cell migration disorder; cell proliferation disorder; neovascularisation;
KW ischaemia; infarction; tissue graft; transplant; human; ephrin-B3;
KW tie receptor tyrosine kinase; Eph receptor ligand.
XX
XX OS Homo sapiens.
XX
XX PN WO2003004529-A2.
XX
XX PD 16-JAN-2003.
XX
XX PF 02-JUL-2002; 2002WO-IB002524.
XX
XX PR 02-JUL-2001; 2001US-0302960P.
XX
XX (LICN ) LICENTIA LTD.
XX
XX PI Alitalo K, Kubo H;
XX
XX DR WPI: 2003-210341/20.
XX DR N-PSDB; ABX12546.
XX
XX Identifying modulators of binding between a Tie receptor tyrosine kinase
PT and an Ephrin ligand, useful for promoting neovascularization, comprises
PT contacting a Tie receptor with an Ephrin in the presence of a putative
PT modulator.
XX
XX PS Disclosure; Page 117-119; 1999p; English.
XX
XX CC The invention describes a method of identifying a modulator of binding
CC between a Tie receptor tyrosine kinase and an Ephrin ligand. The method
CC comprises contacting a Tie receptor composition with an Ephrin
CC composition in the presence and in the absence of a putative modulator
CC compound, and detecting the binding between Tie receptor and the Ephrin
CC in the presence and in the absence of the putative modulator. The method
CC is useful for identifying a modulator of binding between a Tie receptor
CC tyrosine kinase and an Ephrin ligand. Modulators identified from the
CC method are useful in modulating angiogenic processes, including
CC lymphangiogenesis, for creating diseases associated with aberrant Ephrin-
CC Tie biology, aberrant growth, migration or proliferation of cells that
CC express a Tie receptor, or for promoting growth of vessel or
CC neovascularisation (e.g. ischaemic tissue, an infarction, a new or
CC chronic compound, or a tissue graft or transplant). This is the amino
CC acid sequence of human Ephrin-B3, a member of the Ephrin-B subclass of
CC ligands that are bound to the membrane via a transmembrane domain and
CC short cytoplasmic tail and function as Eph receptor ligands
XX
XX Sequence 340 AA;
SQ
Query Match 75.1%; Score 1841; DB 6; Length 340;
Best Local Similarity 100.0%; Pred. No. 4.1e-146;
Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGPPHSGPGGVAVGALLLGLVGLVSGLSLEPYVYNSANKRFOAEGGYLYPOIGDRLDL 60
DB 1 MGPPHSGPGGVAVGALLLGLVGLVSGLSLEPYVYNSANKRFOAEGGYLYPOIGDRLDL 60
QY 61 LCPRARPPGPHSSPNVEFYKYLIVGGAQGRCEAPPAPNLLITCDRDLRFTIKFOEY 120
DB 61 LCPRARPPGPHSSPNVEFYKYLIVGGAQGRCEAPPAPNLLITCDRDLRFTIKFOEY 120
QY 121 SPNLWGHFRSHHDYIITATSDGTREGLESLOGGVCLTGMKYLIRVGQSPRGAVPRKP 180
DB 121 SPNLWGHFRSHHDYIITATSDGTREGLESLOGGVCLTGMKYLIRVGQSPRGAVPRKP 180
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Db 121 SPNLWGEFRSHHDYIIATSDGTREGLSLGGVCLTRGMKYLRLVGQS PRGGAVERPKP 180
 QY 181 VSEMERERGAHSLPEPKENLPDPTSNATSRGAEGLPPSPMPAVAGAGGLALLL 240
 Db 181 VSEMERERGAHSLPEPKENLPDPTSNATSRGAEGLPPSPMPAVAGAGGLALLL 240
 QY 241 GVAGAGGAMCWRRRRAKPSERSRHPGSGFRGGSGLGGGGMGPREAEPGEIGIALRG 300
 Db 241 GVAGAGGAMCWRRRRAKPSERSRHPGSGFRGGSGLGGGGMGPREAEPGEIGIALRG 300
 QY 301 GAADPPCPHYEKVSGDYGHPIYIVODGPPQSPPNIIY 338
 Db 301 GAADPPCPHYEKVSGDYGHPIYIVODGPPQSPPNIIY 338
 RESULT 6
 ADQ21436
 ID ADQ21436 standard; protein; 340 AA.
 AC ADQ21436;
 XX
 XX 26-AUG-2004 (first entry)
 DE Human soft tissue sarcoma-upregulated protein - SEQ ID 4256.
 XX
 KM soft tissue sarcoma; cyclostatic; gene therapy; vaccine; screening; human.
 XX
 OS Homo sapiens.
 XX
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 XX
 PD 26-NOV-2003; 2003WO-US038193.
 PF 26-NOV-2002; 2002US-0429739P.
 PR 26-NOV-2002; 2002US-0429739P.
 XX
 PR (PROT-) PROTEIN DESIGN LABS INC.
 PA Aziz N, Ginsburg WM, Zlotnick A;
 PI WPI; 2004-441208/41.
 DR
 XX
 XX WPI; 2004-441208/41.
 PT Early detection of soft tissue sarcoma comprises determining expression
 PT of a gene in a first soft tissue sample and a normal soft tissue sample
 PT and comparing the gene expression, also useful in treating soft tissue
 PT sarcoma.
 PS
 XX
 PS Example 2; SEQ ID NO 4256; 210pp; English.
 CC The invention relates to a novel method for detecting soft tissue sarcoma
 CC which comprises obtaining a first soft tissue sample from an individual
 CC and a normal soft tissue sample from the same or different individual,
 CC determining the expression of a gene in both samples and comparing the
 CC expression of the gene in both soft tissue samples, where a higher level
 CC of protein expression in the first soft tissue sample indicates the
 CC presence of soft tissue sarcoma. The method of the invention has
 CC cytostatic applications and may be useful for detecting soft tissue
 CC sarcoma, possibly via gene therapy or vaccine production. The nucleic
 CC acid sequences may be useful in diagnostic and screening applications.
 CC The current sequence is that of a human soft tissue sarcoma-upregulated
 CC protein of the invention. The current sequence is not shown within the
 CC specification per se but was submitted in CD format by the inventor.
 CC
 XX
 XX Sequence 340 AA;
 SQ
 Query Match 75.1%; Score 1841; DB 8; Length 340;
 Best Local Similarity 100.0%; Pred No. 4,1e-146;
 Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGPPHSGPGGVRVGVALLLVGLVGLVGLSLPEPVYNNANRRFQAGGGYLYPIQGRDL 60
 Db 1 MGPPHSGPGGVRVGVALLLVGLVGLVGLSLPEPVYNNANRRFQAGGGYLYPIQGRDL 60

QY 61 LCPRARPSPHSSPNVEFYKLYLVGGAQRRCEAPAPNILLTCRPPDLRLFTIKFOEY 120
 Db 61 LCPRARPSPHSSPNVEFYKLYLVGGAQRRCEAPAPNILLTCRPPDLRLFTIKFOEY 120
 QY 121 SPNLWGEFRSHHDYIIATSDGTREGLSLGGVCLTRGMKYLRLVGQS PRGGAVERPKP 180
 Db 121 SPNLWGEFRSHHDYIIATSDGTREGLSLGGVCLTRGMKYLRLVGQS PRGGAVERPKP 180
 QY 181 VSEMERERGAHSLPEPKENLPDPTSNATSRGAEGLPPSPMPAVAGAGGLALLL 240
 Db 181 VSEMERERGAHSLPEPKENLPDPTSNATSRGAEGLPPSPMPAVAGAGGLALLL 240
 QY 241 GVAGAGGAMCWRRRRAKPSERSRHPGSGFRGGSGLGGGGMGPREAEPGEIGIALRG 300
 Db 241 GVAGAGGAMCWRRRRAKPSERSRHPGSGFRGGSGLGGGGMGPREAEPGEIGIALRG 300
 QY 301 GAADPPCPHYEKVSGDYGHPIYIVODGPPQSPPNIIY 338
 Db 301 GAADPPCPHYEKVSGDYGHPIYIVODGPPQSPPNIIY 338
 RESULT 7
 ADY51247
 ID ADY51247 standard; protein; 340 AA.
 AC ADY51247;
 XX
 XX 19-MAY-2005 (first entry)
 DE Human ephrin-B3 SEQ ID NO:16.
 XX
 DE ephrin; hematopoiesis; hyperproliferation; cyclostatic; antianemic;
 KM ephrin; hematopoiesis; hyperproliferation; cyclostatic; antianemic;
 KM coagulant; immunostimulant; cerebroprotective; vasotropic; antitumor.
 XX
 OS Homo sapiens.
 XX
 PN US2005049194-A1.
 PD 03-MAR-2005.
 XX
 PD 31-OCT-2003; 2003US-00638907.
 PF 09-NOV-2001; 2001US-0345206P.
 PR 02-JUL-2002; 2002US-0393272P.
 PR 08-NOV-2002; 2002US-00291290.
 PR 03-APR-2003; 2003US-0460488P.
 XX
 PA (FRIS/) FRISEN J.
 PA (HOLM/) HOLMBERG J.
 PI Friesen J, Holmberg J;
 PI WPI; 2005-195317/20.
 DR
 XX
 XX Use of ephrin and its molecules for alleviating a symptom or a disorder
 PT with reduced levels of hematopoiesis, increased levels of cellular
 PT proliferation in an intestinal tract, or abnormal level of cellular
 PT proliferation in a tissue.
 PS
 PS Disclosure; SEQ ID NO 16; 68pp; English.
 CC The invention relates to a novel use of ephrin, ephrin inhibitors, and
 CC ephrin receptors for alleviating a symptom of a disorder having reduced
 CC levels of hematopoiesis, having increased levels of cellular
 CC proliferation in an intestinal tract, or having an abnormal level of
 CC cellular proliferation in a tissue. A composition of the invention has
 CC cytostatic, antianemic, antiinflammatory, antiproliferative, gastrointest-
 CC -gen, dermatological, coagulant, immunostimulant, cerebroprotective,
 CC vasotropic, and antitumor activity. The present sequence represents
 CC murine ephrin-B3.
 CC
 XX

SQ Sequence 340 AA;
Query Match 75.1%; Score 1841; DB 9; Length 340;
Best Local Similarity 100.0%; Pred. No. 4,1e-146;
Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGPPHSGPGVAVGALLLVGLVGLVSLLEPVYNNNSANKRFOAEGGYLYPQIGDRDL 60
DB 1 MGPPHSGPGVAVGALLLVGLVGLVSLLEPVYNNNSANKRFOAEGGYLYPQIGDRDL 60
QY 61 LCPRARPPGHSSPNVEFYKLYLVGAQGRCEAPAPNLLTCDRPDLDLRTTFKQRY 120
DB 61 LCPRARPPGHSSPNVEFYKLYLVGAQGRCEAPAPNLLTCDRPDLDLRTTFKQRY 120
QY 121 SPNLNGEHRSHHDYIIATSDGTREGLESLOGVCLTRGMKYLTVGQSPRGAVPRKP 180
DB 121 SPNLNGEHRSHHDYIIATSDGTREGLESLOGVCLTRGMKYLTVGQSPRGAVPRKP 180
QY 181 VSEMEMERDRGAHSLPEKKNIPGDPSTNATSRGAEGLPPSPMPAVAGAAAGLALLLL 240
DB 181 VSEMEMERDRGAHSLPEKKNIPGDPSTNATSRGAEGLPPSPMPAVAGAAAGLALLLL 240
QY 241 GVAAGAGAMCWRRRRAKPSRRHPGSGFRGSGSLGLGGGGGMPREARPGELGIALRGG 300
DB 241 GVAAGAGAMCWRRRRAKPSRRHPGSGFRGSGSLGLGGGGGMPREARPGELGIALRGG 300
QY 301 GAADPPFCPHYEKVSGDYGHPIYIVODGPPQSPNNIYY 338
DB 301 GAADPPFCPHYEKVSGDYGHPIYIVODGPPQSPNNIYY 338
RESULT 8
AAW17081
ID AAW17081 standard; protein; 340 AA.
XX AAW17081;
XX 09-AUG-1997 (first entry)
XX EPH family ligand Efl-6.
XX Efl-6; Eph; Elk; receptor tyrosine kinase; signal transduction; ligand;
XX neurological disease.
XX Homo sapiens.
XX OS
XX Key Location/Qualifiers
XX Peptide 1..24
XX /label= Sig_peptide
XX Protein 25..340
XX /label= Mat_protein
XX Misc-difference 166
XX /label= Gln, Arg
XX FT 225..249
XX Domain /label= Transmembrane_domain
XX WO9715667-A1.
XX PN
XX 01-MAY-1997.
XX PD
XX 25-OCT-1996; 96WO-US017201.
XX PF
XX 25-OCT-1995; 95US-0007015P.
XX PR
XX (REGG-) REGENERON PHARM INC.
XX PI Davis S, Gale NW, Yancopoulos GD;
XX MPI; 1997-259021/23.
XX DR N-PSDB; AAT69808.
XX PT New nucleic acid encoding Efl-6 ligand protein - used for promoting
PT growth and proliferation of neuronal cells and in drug screening.

XX Claim 2; Fig 1; 36pp; English.
XX PS
XX A novel ligand (AAW17081), designated Efl-6 (or Eph transmembrane
XX tyrosine kinase family ligand 6), binds to the Elk, Nrk/Cek5, Hek2/Sek4,
XX Hrk and Sek1 receptors on cells. Its amino acid sequence was deduced from
XX a human frontal cortex cDNA clone (AAT69808). Recombinant Efl-6,
XX truncated soluble polypeptides comprising the extracellular domain of Efl-
XX 6, and Efl-6 ligand-binding domains comprising soluble Efl-6 and the FC portion of
XX 19G can be expressed in host cells. These can be used to support neuronal
XX and other Eph receptor-bearing cell populations for treatment of
XX neurological disorders, in drug screening and to raise diagnostic
XX antibodies
SQ Sequence 340 AA;
Query Match 74.9%; Score 1835; DB 2; Length 340;
Best Local Similarity 99.7%; Pred. No. 1.3e-145;
Matches 337; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MGPPHSGPGVAVGALLLVGLVGLVSLLEPVYNNNSANKRFOAEGGYLYPQIGDRDL 60
DB 1 MGPPHSGPGVAVGALLLVGLVGLVSLLEPVYNNNSANKRFOAEGGYLYPQIGDRDL 60
QY 61 LCPRARPPGHSSPNVEFYKLYLVGAQGRCEAPAPNLLTCDRPDLDLRTTFKQRY 120
DB 61 LCPRARPPGHSSPNVEFYKLYLVGAQGRCEAPAPNLLTCDRPDLDLRTTFKQRY 120
QY 61 LCPRARPPGHSSPNVEFYKLYLVGAQGRCEAPAPNLLTCDRPDLDLRTTFKQRY 120
DB 61 LCPRARPPGHSSPNVEFYKLYLVGAQGRCEAPAPNLLTCDRPDLDLRTTFKQRY 120
QY 121 SPNLNGEHRSHHDYIIATSDGTREGLESLOGVCLTRGMKYLTVGQSPRGAVPRKP 180
DB 121 SPNLNGEHRSHHDYIIATSDGTREGLESLOGVCLTRGMKYLTVGQSPRGAVPRKP 180
QY 181 VSEMEMERDRGAHSLPEKKNIPGDPSTNATSRGAEGLPPSPMPAVAGAAAGLALLLL 240
DB 181 VSEMEMERDRGAHSLPEKKNIPGDPSTNATSRGAEGLPPSPMPAVAGAAAGLALLLL 240
QY 241 GVAAGAGAMCWRRRRAKPSRRHPGSGFRGSGSLGLGGGGGMPREARPGELGIALRGG 300
DB 241 GVAAGAGAMCWRRRRAKPSRRHPGSGFRGSGSLGLGGGGGMPREARPGELGIALRGG 300
QY 301 GAADPPFCPHYEKVSGDYGHPIYIVODGPPQSPNNIYY 338
DB 301 GAADPPFCPHYEKVSGDYGHPIYIVODGPPQSPNNIYY 338
RESULT 9
AAW46615
ID AAW46615 standard; protein; 340 AA.
XX AAW46615;
XX 06-JUL-1998 (first entry)
XX Human transmembrane ligand Elk-L3.
XX Elk-L3; Elk-related receptor tyrosine kinase; transmembrane ligand;
XX human; signal transduction; axonogenesis; nerve cell; neurons;
XX Alzheimer's disease; Parkinson's disease; Huntington's disease;
XX demyelination; multiple sclerosis; amyotrophic lateral sclerosis;
XX nervous system infection; Wernicke's disease; trauma; ischaemia; stroke;
XX nutritional polyneuropathy; progressive supranuclear palsy;
XX Shy Drager's syndrome; multistem degeneration;
XX olivoponto cerebellar atrophy; peripheral nerve damage.
XX Homo sapiens.
XX OS
XX Key Location/Qualifiers
XX Peptide 166
XX /label= Gln, Arg
XX FT 225..249
XX Domain /note= "transmembrane domain"
XX WO9801548-A1.
XX PN

XX 15-JAN-1998.
 PD Best Local Similarity 97.6%; Score 1827; DB 2; Length 340;
 PF Matches 336; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 XX 04-JUL-1997; 97WO-CA000473.
 XX 05-JUL-1996; 96US-0021272P.
 XX (MOUN) MOUNT SINAI HOSPITAL CORP.
 XX Holland S, Mbamalu G, Pearson T;
 XX WPI; 1998-101047/09.
 DR N-PSDB; AAV16097.
 XX Modulating transmembrane ligand for an Elk-related receptor tyrosine kinase - by formation of a complex between an oligomerised Elk-related receptor tyrosine kinase and a transmembrane ligand.
 PT
 XX Disclosure; Fig 5A; 40pp; English.

XX This polypeptide comprises human Elk-13, a transmembrane ligand of Elk-related receptor tyrosine kinase (ERK). A novel method of modulating the biological activity of, or for affecting a pathway regulated by, a transmembrane ligand for an ERK in a cell expressing the transmembrane ligand comprises forming a complex between a purified and isolated oligomerised ERK, or an isoform or an extracellular domain of the ERK, and the transmembrane ligand expressed on the cell. The complex can also be used for evaluating a substance for its ability to modulate the biological activity of a transmembrane ligand for an ERK, and to identify substances that affect or modulate a pathway regulated by a ERK. A purified and isolated oligomerised ERK can be used in the preparation of a medicament for modulating neuronal development or regeneration in a subject, or in a medicament for modulating axonogenesis in a subject (all claimed). The substances identified by the methods can be used to modulate axonogenesis, nerve cell interactions and regeneration, to treat diseases and conditions involving trauma and injury to the nervous system, such as Alzheimer's disease, Parkinson's disease, Huntington's disease, demyelinating diseases, such as multiple sclerosis, amyotrophic lateral sclerosis, bacterial and viral infections of the nervous system, deficiency diseases, such as Wernicke's disease and nutritional polyneuropathy, progressive supranuclear palsy, Shy Drager's syndrome, multi-system degeneration and olivoponto cerebellar atrophy, peripheral nerve damage, trauma, and ischaemia resulting from stroke

XX Sequence 340 AA;

Query Match Best Local Similarity 74.6%; Score 1827; DB 2; Length 340;
 Matches 336; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGPPHSGGCVGVGALLLGLVGLVGLSLPEVYNNYNNANKRFOAEGGYLYPOIGRDL 60
 DB 1 MGPPHSGGCVGVGALLLGLVGLVGLSLPEVYNNYNNANKRFOAEGGYLYPOIGRDL 60
 QY 61 LCPRARPPGHSSPNVEFYKLYLVGGAQGRCEAPAPNLLTCDBPDLRTTIKFOEY 120
 DB 61 LCPRARPPGHSSPNVEFYKLYLVGGAQGRCEAPAPNLLTCDBPDLRTTIKFOEY 120
 QY 121 SPNLMGHERSHHDYIYIATSDGTREGLESIGVCLTRGMKYLAVGOSPRGCAVPRXP 180
 DB 121 SPNLMGHERSHHDYIYIATSDGTREGLESIGVCLTRGMKYLAVGOSPRGCAVPRXP 180
 QY 181 VSBMPEMRDGAASHLEPKENLPDPTSNATSRGAEGLPPSPMAVVAAGAGLLALL 240
 DB 181 VSBMPEMRDGAASHLEPKENLPDPTSNATSRGAEGLPPSPMAVVAAGAGLLALL 240
 QY 241 GVAAGAGAACWRRRRKPPSRHPRGSGSLGIGGGCGMPREAPGELGIALRG 300
 DB 241 GVAAGAGAACWRRRRKPPSRHPRGSGSLGIGGGCGMPREAPGELGIALRG 300
 QY 301 GAADPPFCPHYEKVSGDYGHVYIVODGPPQSPNITY 338
 DB 301 GAADPPFCPHYEKVSGDYGHVYIVODGPPQSPNITY 338

DB 301 GAADPPFCPHYEKVSGDYGHVYIVODGPPQSPNITY 338

RESULT 10
 ABU07846
 ID ABU07846 standard; protein; 340 AA.
 XX
 AC ABU07846;
 XX
 DT 10-MAY-2003 (first entry)
 XX
 DE Mouse ephrin-B3 ligand.
 XX
 KW Cytostatic; vasodilator; antiinflammatory; cardiac; gene therapy;
 KW ligand-receptor binding modulator; ephrin ligand; angiogenesis;
 KW lymphangiogenesis; aberrant Ephrin-Tie biology; cell growth disorder;
 KW cell migration disorder; cell proliferation disorder; neovascularisation;
 KW ischaemia; infarction; tissue graft; transplac; mouse; ephrin-B3;
 KW Tie receptor tyrosine kinase; Eph receptor ligand.
 XX

OS Mus musculus.

PN MO2003004529-A2.

PD 16-JAN-2003.

PF 02-JUL-2002; 2002WO-1B002524.

PR 02-JUL-2001; 2001US-0302960P.

PA (LICN) LICENTIA LTD.

PI Alitalo K, Kubo H;

XX WPI; 2003-210341/20.

DR N-PSDB; ABX12547.

XX Identifying modulators of binding between a Tie receptor tyrosine kinase and an Ephrin ligand, useful for promoting neovascularization, comprises contacting a Tie receptor with an Ephrin in the presence of a putative modulator.

XX Disclosure; Page 121-122; 1999p; English.

XX The invention describes a method of identifying a modulator of binding between a Tie receptor tyrosine kinase and an Ephrin ligand. The method comprises contacting a Tie receptor composition with an Ephrin composition in the presence and in the absence of a putative modulator compound, and detecting the binding between the Tie receptor and the Ephrin in the presence and in the absence of the putative modulator. The method is useful for identifying a modulator of binding between a Tie receptor tyrosine kinase and an Ephrin ligand. Modulators identified from the method are useful in modulating angiogenic processes, including lymphangiogenesis, for treating diseases associated with aberrant Ephrin-Tie biology, aberrant growth, migration or proliferation of cells that express a Tie receptor, or for promoting growth of vessel or neovascularisation (e.g. ischaemic tissue, an infarction, a new or chronic compound, or a tissue graft or transplant). This is the amino acid sequence of mouse Ephrin-B3, a member of the Ephrin-B subclass of ligands that are bound to the membrane via a transmembrane domain and short cytoplasmic tail and function as Eph receptor ligands

XX Sequence 340 AA;

Query Match Best Local Similarity 72.3%; Score 1771; DB 6; Length 340;
 Matches 323; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 MGPPHSGGCVGVGALLLGLVGLVGLSLPEVYNNYNNANKRFOAEGGYLYPOIGRDL 60
 DB 1 MGPPHSGGCVGVGALLLGLVGLVGLSLPEVYNNYNNANKRFOAEGGYLYPOIGRDL 60
 QY 61 LCPRARPPGHSSPNVEFYKLYLVGGAQGRCEAPAPNLLTCDBPDLRTTIKFOEY 120
 DB 61 LCPRARPPGHSSPNVEFYKLYLVGGAQGRCEAPAPNLLTCDBPDLRTTIKFOEY 120

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Db      61 LCPRAAPPCHSSPSYEFKLYLVEGAQGRCEAPPAPNLLITCDRPDIDLRTTIKFOEY 120
QY      121 SPNLWGEHRSRHHDDYIIATSDGTREGLESLOGVCLTRGMKVLRLVGOSPRGAVPRRP 180
Db      121 SPNLWGEHRSRHHDDYIIATSDGTREGLESLOGVCLTRGMKVLRLVGOSPRGAVPRRP 180
QY      181 VSEMERDRGAASHLEPGKENLPGDPTSNATSRGAEGPLPPSPMPAVAGAAGLALLLL 240
Db      181 VSEMERDRGAASHLEPGKENLPGDPTSNATSRGAEGPLPPSPMPAVAGAAGLALLLL 240
QY      241 GVAAGAGAMCWRRRRAKPSERHPPGSGFRGSGSLGGGGGMGPREAPPGELGIALRGG 300
Db      241 GVAAGAGAMCWRRRRAKPSERHPPGSGFRGSGSLGGGGGMGPREAPPGELGIALRGG 300
QY      301 GAADPPFCPHYEKVSGDYGHPIYIVODGPPQSPPNIIY 338
Db      301 GTADPPFCPHYEKVSGDYGHPIYIVODGPPQSPPNIIY 338

```

RESULT 11
ADY51239
ID ADY51239 standard; protein; 340 AA.

AC ADY51239;
DT 19-MAY-2005 (first entry)
DE Mouse ephrin-B3 SEQ ID NO:8.

XX ephrin; hematopoiesis; hyperproliferation; cytostatic; antiamebic;
XX antinflammatory; antiproliferative; gastrointestinal-gen.; dermatological;
XX coagulant; immunostimulant; cerebroprotective; vasotropic; antitumor.

OS Mus musculus.

PN US2005049194-A1.

PD 03-MAR-2005.

PF 31-OCT-2003; 2003US-00698907.

PR 09-NOV-2001; 2001US-0345206P.

PR 02-JUL-2002; 2002US-0393272P.

PR 08-NOV-2002; 2002US-00291290.

PR 03-APR-2003; 2003US-0460488P.

XX (FRIS/) FRISSEN J.

XX (HOLM/) HOLMBERG J.

XX Friese J., Holmberg J.

XX MPI; 2005-195317/20.

XX Use of ephrin and its molecules for alleviating a symptom or a disorder

XX with reduced levels of hematopoiesis, increased levels of cellular

XX proliferation in an intestinal tract, or abnormal level of cellular

XX proliferation in a tissue. A composition of the invention has

XX cytostatic, antiamebic, antinflammatory, antiproliferative, gastrointestinal

XX -gen., dermatological, coagulant, immunostimulant, cerebroprotective,

XX vasotropic, and antitumor activity. The present sequence represents

XX murine ephrin-B3.

XX Sequence 340 AA;

Query Match 72.3%; Score 1771; DB 9; Length 340;
Best Local Similarity 95.6%; Pred. No. 3.2e-140;
Matches 323; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

```

QY      1 MCPHSGPGVAVGALLLGLVGLVSLSEPVYNNNSANKRFQAGGYLYFQIGDRDL 60
Db      1 MCPHSGPGVAVGALLLGLVGLVSLSEPVYNNNSANKRFQAGGYLYFQIGDRDL 60
QY      61 LCPRAAPPCHSSPSYEFKLYLVEGAQGRCEAPPAPNLLITCDRPDIDLRTTIKFOEY 120
Db      61 LCPRAAPPCHSSPSYEFKLYLVEGAQGRCEAPPAPNLLITCDRPDIDLRTTIKFOEY 120
QY      121 SPNLWGEHRSRHHDDYIIATSDGTREGLESLOGVCLTRGMKVLRLVGOSPRGAVPRRP 180
Db      121 SPNLWGEHRSRHHDDYIIATSDGTREGLESLOGVCLTRGMKVLRLVGOSPRGAVPRRP 180
QY      181 VSEMERDRGAASHLEPGKENLPGDPTSNATSRGAEGPLPPSPMPAVAGAAGLALLLL 240
Db      181 VSEMERDRGAASHLEPGKENLPGDPTSNATSRGAEGPLPPSPMPAVAGAAGLALLLL 240
QY      241 GVAAGAGAMCWRRRRAKPSERHPPGSGFRGSGSLGGGGGMGPREAPPGELGIALRGG 300
Db      241 GVAAGAGAMCWRRRRAKPSERHPPGSGFRGSGSLGGGGGMGPREAPPGELGIALRGG 300
QY      301 GAADPPFCPHYEKVSGDYGHPIYIVODGPPQSPPNIIY 338
Db      301 GTADPPFCPHYEKVSGDYGHPIYIVODGPPQSPPNIIY 338

```

RESULT 12
ADJ70889
ID ADJ70889 standard; protein; 285 AA.

AC ADJ70889;
DT 06-MAY-2004 (first entry)

DE Human heat mitochondrial protein as a therapeutic target SeqID2695.

XX mitochondrial; human; screening assay; diabetes mellitus;

XX Huntington's disease; osteoarthritis;

XX Leber's hereditary optic neuropathy; LHON;

XX mitochondrial encephalopathy lactic acidosis and stroke; MELAS;

XX myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;

XX neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;

XX osteopathic; ophthalmological; cytostatic.

XX Homo sapiens.

XX WO2003087768-A2.

XX 23-OCT-2003.

XX 04-APR-2003; 2003WO-US010870.

XX 12-APR-2002; 2002US-0372843P.

XX 17-JUN-2002; 2002US-0389987P.

XX 20-SEP-2002; 2002US-0412418P.

XX (MITO-) MITOXOR.

XX (BUCK-) BUCK INST AGE RES.

XX Ghosh SS, Fahy BD, Zhang B, Gibson BW, Taylor SW, Glenn GM,

XX Warnock DE;

XX MPI; 2003-845369/78.

XX Identifying a mitochondrial target for drug screening assays and for

XX treating diseases associated with altered mitochondrial function,

XX comprises detecting a modified polypeptide in a sample and correlating

XX with the disease.

XX Claim 1; SEQ ID NO 2695; 1800pp; English.

XX This invention relates to novel mitochondrial targets that can be used
 CC for therapeutic intervention in treating a disease associated with
 CC altered mitochondrial function. Specifically, it refers to a method for
 CC identifying proteins of the human heart mitochondrial proteome that are
 CC useful for drug screening assays, as well as therapeutic targets. The
 CC present invention describes a method for identifying such proteins that
 CC can be used in the treatment of various diseases associated with altered
 CC mitochondrial function including diabetes mellitus, Huntington's disease,
 CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
 CC encephalopathy, lactic acidosis and stroke (MELAS), myoclonic epilepsy
 CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
 CC compositions have neuroprotective, nootropic, antidiabetic,
 CC anticonvulsant, antiarrhythmic, osteopathic, ophthalmological and
 CC cyostatic activities. This polypeptide sequence is a human heart
 CC mitochondrial protein of the invention.

XX Sequence 285 AA;

SQ Query Match 63.3%; Score 1550; DB 7; Length 285;

Best Local Similarity 100.0%; Pred. No. 9,8e-122; Indels 0; Gaps 0;

Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 DELDLCPRARPPGHSPPNYEFYKYLIVGAQGRRCBAPAPNLLTCDRDLRLFTI 115

DB 1 DRDLCLCPARPPGHSPPNYEFYKYLIVGAQGRRCBAPAPNLLTCDRDLRLFTI 60

QY 116 KFOEISPNMGHEFSSHDIYIATSDGTREGLESIGGVCITRGKVLRLVQGSRRGA 175

DB 61 KFOEISPNMGHEFSSHDIYIATSDGTREGLESIGGVCITRGKVLRLVQGSRRGA 120

QY 176 VPRKVSSEMPERDGAHSLRPGKENTLPGDPTSNATSGAEGPLPPSPMAVAGAAGL 235

DB 121 VPRKVSSEMPERDGAHSLRPGKENTLPGDPTSNATSGAEGPLPPSPMAVAGAAGL 180

QY 236 ALLLGVAGAGAMCRRRRRAKPSRRHPPGSPFGSGSLGGGGGMGPRAEPDELGI 295

DB 181 ALLLGVAGAGAMCRRRRRAKPSRRHPPGSPFGSGSLGGGGGMGPRAEPDELGI 240

QY 236 ALRGGGADPPFCPHYEKVSGDYGHVYIVODGPPSPNIIY 338

DB 241 ALRGGGADPPFCPHYEKVSGDYGHVYIVODGPPSPNIIY 283

RESULT 13

AAW00287 standard; protein; 334 AA.

AC AAW00287;

XX 19-JAN-1997 (first entry)

DE Mouse Eph receptor ligand ELF-2.

XX Eph receptor; ligand; ELF-2; tyrosine kinase; signal transduction;

KW organogenesis; oncogenesis; tumour; neurological disorder; diagnosis;

KM gene therapy.

XX Mus sp.

OS Mus sp.

XX Key Location/Qualifiers

FT Domain 1..224

FT Binding-site 31..155

FT Domain 226..251

XX WO9626958-A2.

XX 06-SEP-1996.

XX 23-FEB-1996; 96WO-US002673.

XX 27-FEB-1995; 95US-00395415.
 PR (HARD) HARVARD COLLEGE.
 XX Flanagan JG, Bergemann AD;
 PI WPI; 1996-43391/43.
 DR N-PSDB; AAT40230.

XX Efn receptor ligand, ELF-2, and DNA encoding it - used to treat or

PT prevent neurological diseases, and to modulate binding of ELF-2 to Efn

PS receptor, e.g. to prevent or treat tumour formation.

XX Claim 6; Fig 1A-B; 50pp; English.

XX Mouse Eph receptor ligand ELF-2 (AAW00287) is strongly expressed in the

CC anterior hindbrain and newly-forming somites of embryos at the early

CC organogenesis stage of development. It is important in cellular

CC communication during pattern formation. Its amino acid sequence was

CC deduced from a cDNA clone (AAT40230) isolated from a newborn mouse brain

CC cDNA library. The ELF-2 ligand can be used to alter neurological

CC development, oncogenesis and growth regulation, to modulate binding of

CC ELF-2 to the Efn receptor, and in diagnostic assays

SQ Sequence 334 AA;

QY 14 GALLLVGLVLSGLSEPVNNSANKRFOAGGVLYPQIGDRDLCLCPRARPPGHS 73

DB 15 GLLMLCRAIIRSYLSEPIYNNSSKFLPGQGLVLYPQIGDKDILCPK---DSKTY 71

QY 74 PNYEFYKYLIVGAQGRRCBAPAPNLLTCDRDLRLFTIKFOEISPNMGHEFSSH 133

DB 72 GQYEVYKVMVDKQADRCTIKENTPLNLCARPDQDVFTIKFOEISPNMGLEFQK 131

QY 134 DYIITATSDGTREGLESIGGVCITRGKVLRLVQGSRRGA--SPRGAYPRKVSSEMPER-DR 190

DB 132 DYIITATSDGTREGLESIGGVCITRGKVLRLVQGSRRGA--SPRGAYPRKVSSEMPER-DR 191

QY 191 GAHSLRPGKENTLPGDPTSNATSGAEGPLPPSPMAVAGAAGLALLLGVAGAGAMC 250

DB 192 GRSSTSPVKNPPGSPSTGNSAGSNNLLSEVALFPGIAGSCIPIVITLVLL 251

QY 251 WRRRAKPSRRHPPGSPFGSGSLGGGGGMGPRAEPDELGIALRGGGADPPFCPH 310

DB 252 KYRRRRHKHSPOHTTTLSLTATPRGNN---NGSEPSDVIIPLR---TADSVFCPH 304

QY 311 YEKVSGDYGHVYIVODGPPSPNIIY 338

DB 305 YEKVSGDYGHVYIVODGPPSPNIIY 332

RESULT 14

AAW00287 standard; protein; 336 AA.

AC AAR92742;

XX 21-MAY-1996 (first entry)

DE Murine hepatoma transmembrane kinase receptor ligand.

XX Hepatoma transmembrane kinase; Htk; receptor; ligand; tyrosine kinase;

XX neurodegenerative disease.

XX Mus musculus.

XX WO9602645-A2.

PD 01-FEB-1996.
XX
XX 14-JUL-1995; 95WO-US008812.
XX
XX 20-JUL-1994; 94US-00277722.
XX
XX (GETH) GENENTECH INC.
XX
XX Bennett BD, Matthews W;
XX
XX MPI, 1996-105907/11.
DR N-PEDB; AAT16470.
XX
XX ligand for the hepatoma trans-membrane kinase receptor - useful for
PT stimulating and inhibiting cells carrying the receptor, e.g. for treating
PT neuro-degenerative disease.
XX
XX Claim 5; fig 1(A-D); 88pp; English.
XX
XX Mouse (AAT16470) and human (AAT16471) Htk ligand which bind to, and
CC activate, the Htk receptor, have been identified in a variety of tissues
CC using a soluble Htk-PC fusion protein. The predicted mol.wt. of the
CC murine Htk ligand protein following a signal peptide cleavage is 34 kD
CC with an estimated pI of 8.9. The murine and human ligands show 96%
CC homology at the amino acid level. The DNA is used to produce recombinant
CC ligands; for tissue-specific typing (partic. as a marker for breast
CC cancer) and as a marker for human chromosome 13. The ligands (partic. in
CC soluble form) are used to activate the tyrosine kinase domain of the Htk
CC receptor, i.e. to stimulate or inhibit growth, differentiation, and/or
CC activation of cells contg. the receptor, e.g. treatment of
CC neurodegenerative diseases, since they are strongly expressed in the
CC cerebral cortex, hippocampus, striatum and cerebellum. The ligands are
CC also useful as a control or standard in assays, for generation of
CC antibodies, as a mol. wt. marker, for growth in vitro of Htk-receptor
CC positive cells, as research agent, in screening, etc
XX
XX Sequence 336 AA;
SQ
Query Match 25.7%; Score 628.5; DB 2; Length 336;
Best Local Similarity 41.8%; Pred. No. 3.8e-44;
Matches 137; Conservative 49; Mismatches 129; Indels 13; Gaps 5;
OY 14 GALLILGLVLSGSLSEPPVWNSANKRFOAGGYLVLPQIGDRDLDCPRARPPGPHSS 73
DB 17 GLMWLCRTAISRSIVLEPIYWNSSNSKFLPQGLVLPQIGDKLDICPKV---DSKTV 73
OY 74 PNYEFYKUYLVGAGRGRCRAPNLLTCDRPLDLRFTIKRQEXSPNLMGHEFRSHH 133
DB 74 GQYEFYKUYMWVDKDDADRCTTKENTPILNCRPDDVAFYTIKFQFSPNLMGLEFQKK 133
OY 134 DYYIATSDGTREGLESLOGVCLTRGMKVLRLVGO--SPRCGAVPRKPVSEMPMER-DR 190
DB 134 DYYIISTNGSLGEGDNGEGVCQTRAMKILMKVQDASASANNHGTRRELEAGTN 193
OY 191 GAHSLPEGKENTLPGDPTSNATSRGAEGLPPSPMPAVAGAAGLALLILGVAGAGAMC 250
DB 194 GRSSTSPFVKPNPSSSTIDGNSAGSNNLLGSEVALFAGIASGCIIFIVIIITLVVLL 253
OY 251 WRRRAKSESSEHHPGSGFRGSGSLGCGGGMGRREAPGLGIALRGGGAADPPFCN 310
DB 254 KYRRHRKHSPOHTTTLSLTATPRGGNN---NGSEPSDVIILPLR--TADSVFCH 306
OY 311 YEKVSGDYGHPPYIVODGPPGSPPNIIY 338
DB 307 YEKVSGDYGHPPYIVODGPPGSPPNIIY 334
RESULT 15
ADYS1238
ID ADV51238 standard; protein; 336 AA.
XX
XX ADV51238;
XX

DT 19-MAY-2005 (first entry)
XX
XX Mouse ephrin-B2 SEQ ID NO:7.
DE
XX ephrin; hematopoiesis; hyperproliferation; cytosstatic; antiandemic;
XX antinflammatory; antiporiatic; gastrointestinal-gen.; dermatological;
KM coagulant; immunostimulant; cerebroprotective; vasotropic; antitumor.
XX
XX Mus musculus.
OS
XX
XX Key Location/Qualifiers
FH Misc-difference 2.3
FT /note= "Optionally deleted"
FT
XX US2005049194-A1.
XX
XX 03-MAR-2005.
XX
XX 31-OCT-2003; 2003US-00698907.
XX
XX 09-NOV-2001; 2001US-0345206P.
PR 02-JUL-2002; 2002US-0393272P.
PR 08-NOV-2002; 2002US-00291290.
PR 03-APR-2003; 2003US-0460488P.
XX
XX (FRIS/) FRISEN J.
PA (HOLM/) HOLMBERG J.
XX
XX Frisen J, Holmberg J;
XX
XX MPI, 2005-195317/20.
XX
XX Use of ephrin and its molecules for alleviating a symptom or a disorder
PT with reduced levels of hematopoiesis, increased levels of cellular
PT proliferation in an intestinal tract, or abnormal level of cellular
PT proliferation in a tissue.
XX
XX Disclosure; SEQ ID NO 7; 68pp; English.
XX
XX The invention relates to a novel use of ephrin, ephrin inhibitors, and
XX ephrin receptors for alleviating a symptom of a disorder having reduced
XX levels of hematopoiesis, having increased levels of cellular
XX proliferation in an intestinal tract, or having an abnormal level of
XX cellular proliferation in a tissue. A composition of the invention has
XX cytosstatic, antiandemic, antiporiatic, antiporiatic, gastrointestinal
XX -gen., dermatological, coagulant, immunostimulant, cerebroprotective,
XX vasotropic, and antitumor activity. The present sequence represents
XX murine ephrin-B2.
XX
XX Sequence 336 AA;
SQ
Query Match 25.7%; Score 628.5; DB 9; Length 336;
Best Local Similarity 41.8%; Pred. No. 3.8e-44;
Matches 137; Conservative 49; Mismatches 129; Indels 13; Gaps 5;
OY 14 GALLILGLVLSGSLSEPPVWNSANKRFOAGGYLVLPQIGDRDLDCPRARPPGPHSS 73
DB 17 GLMWLCRTAISRSIVLEPIYWNSSNSKFLPQGLVLPQIGDKLDICPKV---DSKTV 73
OY 74 PNYEFYKUYLVGAGRGRCRAPNLLTCDRPLDLRFTIKRQEXSPNLMGHEFRSHH 133
DB 74 GQYEFYKUYMWVDKDDADRCTTKENTPILNCRPDDVAFYTIKFQFSPNLMGLEFQKK 133
OY 134 DYYIATSDGTREGLESLOGVCLTRGMKVLRLVGO--SPRCGAVPRKPVSEMPMER-DR 190
DB 134 DYYIISTNGSLGEGDNGEGVCQTRAMKILMKVQDASASANNHGTRRELEAGTN 193
OY 191 GAHSLPEGKENTLPGDPTSNATSRGAEGLPPSPMPAVAGAAGLALLILGVAGAGAMC 250
DB 194 GRSSTSPFVKPNPSSSTIDGNSAGSNNLLGSEVALFAGIASGCIIFIVIIITLVVLL 253
OY 251 WRRRAKSESSEHHPGSGFRGSGSLGCGGGMGRREAPGLGIALRGGGAADPPFCN 310
XX
XX

Db 254 KYRRHRKHSPOHTTTLSTLATPRGNN---NGSESDVILPLR---TADSVFCPH 306
OY 311 YEKVSGDYGHPPYIYVODGPPSPNNIY 338
| | | | | | | | | | : | | | | |
Db 307 YEKVSGDYGHPPYIYVODGPPSPNNIY 334

Search completed: December 21, 2005, 14:30:18
Job time : 156.239 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 21, 2005, 14:17:53 ; Search time 113.761 Seconds
(without alignments)
1313.181 Million cell updates/sec

Title: US-10-021-121-4

Perfect score: 1850
Sequence: 1 MGPSPSGPGVAVGALLLG.....PVTVDGPPSPNYYKV 340

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A_Geneseq_21.*
1: geneseqp1980s:*
2: geneseqp1980s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1850	100.0	340	2	AAW31544 Human cye
2	1850	100.0	340	2	AAW33699 AL-2-bhor
3	1850	100.0	340	2	AAW10637 NLERK2 11
4	1850	100.0	340	6	ABU07845 Human eph
5	1850	100.0	340	8	ADQ21436 Human eph
6	1850	100.0	340	9	ADY51247 Human eph
7	1844	99.7	340	2	AAW17081 EPH fam1
8	1841	99.5	455	2	AAW33698 AL-2-long
9	1836	99.2	340	2	AAW46615 Human tra
10	1780	96.2	340	6	ABU07846 Mouse eph
11	1780	96.2	340	9	ADY51239 Mouse eph
12	1559	84.3	285	7	ADJ70889 Human hea
13	637.5	34.5	334	2	AAW00287 Mouse eph
14	637.5	34.5	336	2	AAW2742 Murine he
15	637.5	34.5	336	9	ADY51238 Mouse eph
16	635.5	34.4	336	6	ABU07844 Mouse eph
17	632	34.2	346	2	AAW5059 ELK tyros
18	632	34.2	346	2	AAW1930 Human cye
19	632	34.2	346	2	AAW19249 Human eph
20	632	34.2	346	2	AAW36055 Human eph
21	632	34.2	346	6	AAW44323 Human eph
22	632	34.2	346	6	ABU07841 Human eph
23	632	34.2	346	7	ABU62401 Human eph
24	632	34.2	346	7	ADN95630 Human BEC

25	632	34.2	346	8	ADH76244 Human nov
26	632	34.2	346	8	ADO28631 Human eph
27	632	34.2	346	8	ADR73462 Human eph
28	632	34.2	346	9	ADY97175 Human eph
29	632	34.2	346	9	ADY51245 Human eph
30	631	34.1	346	2	AAW82606 Eph trans
31	630.5	34.1	331	2	AAW00288 Chicken E
32	629.5	34.0	333	2	AAW94655 Ligand fo
33	629.5	34.0	333	2	AAW92743 Human hep
34	629.5	34.0	333	2	AAW89287 Human LER
35	629.5	34.0	333	2	AAW06337 Full leng
36	629.5	34.0	333	6	AAW11308 Receptor-
37	629.5	34.0	333	6	ABU07886 Novel hum
38	629.5	34.0	333	7	ADN03886 Antipepti
39	629.5	34.0	333	8	ADP26886 Human eph
40	629.5	34.0	333	8	ADP67298 Human bla
41	629.5	34.0	333	8	ADR86706 Human eph
42	629.5	34.0	333	8	ADR82653 Human eph
43	629.5	34.0	333	9	ADV73221 Human col
44	629.5	34.0	333	9	ADY51246 Human eph
45	629.5	34.0	333	9	ADY51246 Human eph

ALIGNMENTS

RESULT 1	AAW31544	AAW31544 standard; protein, 340 AA.
XX	XX	AAW31544;
AC	XX	14-APR-1998 (first entry)
XX	XX	Human cytokine Lerk-8.
DE	XX	Lerk-8; cytokine; human; hek; elk; receptor tyrosine kinase; ligand;
XX	XX	KW neurodegenerative disease; wound healing; neovascularization; diagnosis;
KW	XX	therapy.
XX	XX	Homo sapiens.
OS	XX	Location/Qualifiers
XX	XX	1..27
XX	XX	/label= Sig_peptide
FT	FT	28..340
FT	FT	/label= Mat_protein
FT	FT	28..224
FT	FT	/note= "extracellular domain"
FT	FT	210..212
FT	FT	/note= "n-glycosylated"
FT	FT	225..251
FT	FT	/note= "transmembrane domain"
FT	FT	252..340
FT	FT	/note= "cytoplasmic domain"
FT	FT	325
FT	FT	/note= "residue 325 is Leu in Lerk-8 variant"
XX	XX	WO9736919-A2.
XX	XX	09-OCT-1997.
XX	XX	19-MAR-1997; 97WO-US004533.
XX	XX	21-MAR-1996; 96US-00621146.
XX	XX	(IMMV) IMMUNEX CORP.
XX	XX	Cerretti DP;
XX	XX	WPI; 1997-503043/46.
XX	XX	N-PSDB; AAT89519.

PT New isolated cytokine, Ierk-8 - binds to the hek and elk receptor
 PT tyrosine kinases, used to develop products for diagnosis and therapy.
 XX
 PS Claim 3; Page 32-33; 37pp; English.

CC This protein sequence comprises a novel human cytokine designated Ierk-8.
 CC The amino acid sequence was deduced from a human foetal brain cDNA clone
 CC (see AA899519). Ierk-8 binds to the cell surface receptors hek and elk,
 CC which are members of the eph/elk family of receptor tyrosine kinases.
 CC Ierk-8 polypeptides, especially soluble polypeptides comprising amino
 CC acid residues 27 to 142-197 of the full-length protein, can be expressed
 CC in transformed host cells. These polypeptides can be used to purify hek
 CC or elk proteins, and to purify or identify cells that express hek or elk
 CC on the surface. Such cells can be used in various *in vitro* studies or *in*
 CC *vivo* procedures, e.g. neural cells expressing elk can be administered to
 CC a mammal afflicted with a neurodegenerative disorder. The Ierk-8
 CC polypeptides can also be used to deliver diagnostic or therapeutic agents
 CC to these cells (e.g. leukaemia cells). The Ierk-8 DNA and polypeptides
 CC can also be used to: treat disorders mediated by defective or
 CC insufficient amounts of Ierk-8; to treat disorders such as injury to
 CC neural tissue or neurological disease; to promote angiogenesis; and for
 CC wound healing or stimulating neovascularisation of grafted tissues

XX Sequence 340 AA;

Query Match 100.0%; Score 1850; DB 2; Length 340;
 Best Local Similarity 100.0%; Pred. No. 2.5e-142;
 Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGPPHSGPGGVAVGALLLIGVLTGLVSGLSLEPYVYNSANKRFOAEGGYLYPOIGRDL 60
 DB 1 MGPPHSGPGGVAVGALLLIGVLTGLVSGLSLEPYVYNSANKRFOAEGGYLYPOIGRDL 60
 QY 61 LCPRRAPPBGHSSPNVEFYKLYLVGAQGRCEAPAPAPMLLTCDPDDDLRTTFKFOEY 120
 DB 61 LCPRRAPPBGHSSPNVEFYKLYLVGAQGRCEAPAPAPMLLTCDPDDDLRTTFKFOEY 120
 QY 121 SPNLMGHEFRSHHDYIIATSDGTREGLESLOGVCLTRGMKVLTVGSGPRGAVPRKP 180
 DB 121 SPNLMGHEFRSHHDYIIATSDGTREGLESLOGVCLTRGMKVLTVGSGPRGAVPRKP 180
 QY 181 VSEMPMERDRGAHSLPEKKNLPDPTSNATSRGAEGLPPPSMVAVGAAGLALLLL 240
 DB 181 VSEMPMERDRGAHSLPEKKNLPDPTSNATSRGAEGLPPPSMVAVGAAGLALLLL 240
 QY 241 GVAAGAGACWRRRAKPSBSRHGPGSGFERGSLGLGGGCGMPREABPGEILRG 300
 DB 241 GVAAGAGACWRRRAKPSBSRHGPGSGFERGSLGLGGGCGMPREABPGEILRG 300
 QY 301 GAADPPFCPHYEKVSGDYGVYITVDGPQSPNNIYKY 340
 DB 301 GAADPPFCPHYEKVSGDYGVYITVDGPQSPNNIYKY 340

RESULT 2
 AAM33699
 ID AAM33699 standard; protein; 340 AA.

XX AAM33699;
 AC AAM33699;
 DT 30-APR-1998 (first entry)
 XX
 DE AL-2-short (AL-2s) protein.
 XX

KM AL-2s; AL-2; AL-2-short; human; treatment; neurological disorder; tumour;
 KM rheumatoid arthritis; wound healing; paralysis; angiogenesis; leukaemia;
 KM psoriasis; Alzheimer's disease; epilepsy.

XX Homo sapiens.
 OS
 FH Key Location/Qualifiers
 FT Peptide 1..26
 FT /note="signal peptide"

FT Protein 27..340
 FT /note="mature protein"
 FT Domain 27..219
 FT /note="extracellular domain"
 FT Domain 220..245
 FT /note="hydrophobic transmembrane domain"

XX MO9740153-A1.
 XX 30-OCT-1997.
 PD

PF 17-APR-1997; 97MO-US006345.
 XX

PR 19-APR-1996; 96US-00635130.
 XX

PA (GENT) GENENTECH INC.
 XX

PI Caras IW;
 XX

XX WPI; 1997-535837/49.
 DR

DR N-PSDB; AAV06355.
 XX

PT Human AL-2 neurotrophic factor and related DNA - used to develop products
 PT for, e.g. treating neurologic disorders, angiogenesis disorders, tumours
 PT or rheumatoid arthritis or for wound healing.

PS Claim 20; Fig 2A-B; 86pp; English.

CC This is a AL-2-short (AL-2s) protein. The AL-2 is a novel Eph-related
 CC tyrosine kinase receptor ligand. AL-2 can be administered to patients in
 CC whom the nervous system has been damaged by trauma, surgery, stroke,
 CC ischaemia, infection, metabolic disease, nutritional deficiency,
 CC malignancy, or toxic agents, to promote the survival or growth of
 CC neurons. They can be used to treat motoneuron disorders such as
 CC amyotrophic lateral sclerosis (Lou Gehrig's disease), Bell's palsy, and
 CC various conditions involving spinal muscular atrophy, or paralysis. AL-2
 CC can be used to treat human neurodegenerative disorders, such as
 CC Alzheimer's disease, Parkinson's disease, epilepsy, demyelinating
 CC diseases such as multiple sclerosis, Huntingtons chorea, Down's syndrome,
 CC nerve deafness, Menier's disease, and other disorders of the cerebellum.
 CC AL-2 can be used as cognitive enhancer, to enhance learning particularly
 CC in dementias or trauma, since they can promote axonal outgrowth and
 CC synaptic plasticity, particularly of hippocampal neurons that express AL-
 CC 2 binding Eph-family receptors and cortical neurons that express AL-2. AL-
 CC -2 can also be used for wound healing, i.e. accelerating
 CC neovascularisation of, e.g. burns and ulcers. The encoding nucleic acids
 CC are useful in preparing antibodies that specifically bind to the AL-2
 CC protein. The antibodies and the AL-2 antagonists are useful in diagnosing
 CC and treating various neuronal disorders. AL-2 antagonists can be used for
 CC modulating angiogenesis. They can also be used for the treatment of
 CC tumours, acute myeloid leukaemia (AML), chronic myeloid leukaemia (CML),
 CC myelodysplastic syndrome (MDS), diabetic retinopathy, neovascular
 CC glaucoma, psoriasis and rheumatoid arthritis

XX Sequence 340 AA;

Query Match 100.0%; Score 1850; DB 2; Length 340;
 Best Local Similarity 100.0%; Pred. No. 2.5e-142;
 Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGPPHSGPGGVAVGALLLIGVLTGLVSGLSLEPYVYNSANKRFOAEGGYLYPOIGRDL 60
 DB 1 MGPPHSGPGGVAVGALLLIGVLTGLVSGLSLEPYVYNSANKRFOAEGGYLYPOIGRDL 60
 QY 61 LCPRRAPPBGHSSPNVEFYKLYLVGAQGRCEAPAPAPMLLTCDPDDDLRTTFKFOEY 120
 DB 61 LCPRRAPPBGHSSPNVEFYKLYLVGAQGRCEAPAPAPMLLTCDPDDDLRTTFKFOEY 120
 QY 121 SPNLMGHEFRSHHDYIIATSDGTREGLESLOGVCLTRGMKVLTVGSGPRGAVPRKP 180
 DB 121 SPNLMGHEFRSHHDYIIATSDGTREGLESLOGVCLTRGMKVLTVGSGPRGAVPRKP 180
 QY 181 VSEMPMERDRGAHSLPEKKNLPDPTSNATSRGAEGLPPPSMVAVGAAGLALLLL 240
 DB 181 VSEMPMERDRGAHSLPEKKNLPDPTSNATSRGAEGLPPPSMVAVGAAGLALLLL 240

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Db      181 VSEMPERDRGAHSLPEKENVLPDPTSNATSRGAEGLPPPSMPAVAVGAAGLALLLL 240
Qy      241 GVAAGAGAMCWMRRRAKPSRSSHPGSGFGRGSLGLGGGGMGPREAPPELGIALRG 300
Db      241 GVAAGAGAMCWMRRRAKPSRSSHPGSGFGRGSLGLGGGGMGPREAPPELGIALRG 300
Qy      301 GAADPPFCPHYEKVSGDYGHPIYIVODGPPQSPPNITYYKV 340
Db      301 GAADPPFCPHYEKVSGDYGHPIYIVODGPPQSPPNITYYKV 340

RESULT 3
AAW10637
ID      AAW10637 standard; protein; 340 AA.
XX      AAW10637;
XX      AAW10637;
XX      23-JUN-1997 (first entry)
XX      NLERK2 ligand for eph-related kinase.
XX      NLERK2 ligand for eph-related kinase.
XX      LERK; ligand for eph-related kinase; ERK; NLERK2;
XX      KW receptor protein tyrosine kinase; cell proliferation;
XX      cell differentiation; cell survival; nerve cell.
XX      Homo sapiens.
XX      Key
XX      Location/Qualifiers
XX      Peptide
XX      1..29
XX      /label= Sig_peptide
XX      Protein
XX      30..340
XX      /label= Mat_protein
XX      Modified-site
XX      210
XX      /label= N-glycosylation_site
XX      227..251
XX      /label= Transmembrane_domain
XX      Domain
XX      W09704091-A1.
XX      19-JUL-1996; 96WC-AU000460.
XX      06-FEB-1997.
XX      20-JUL-1995; 95AU-00004263.
XX      27-NOV-1995; 95AU-00006847.
XX      22-DEC-1995; 95AU-00007299.
XX      05-FEB-1996; 96AU-00007890.
XX      (AMRA-) AMRAD OPERATIONS PTY LTD.
XX      Nicola NA;
XX      WPI; 1997-132632/12.
XX      N-PSDB; AAT60966.
XX      Nucleic acid mol. encoding ligand for eph-related kinase - useful for
XX      treatment of, pret. neuronal, cells to increase survival, proliferation
XX      and differentiation.
XX      Claim 16; Page 37-39; 71pp; English.
XX      A novel human ligand for eph-related kinase (LERK) is designated NLERK2
XX      (AAW10637). It is encoded by a cDNA clone (AAT60966) obtd. from a human
XX      foetal brain cDNA library. The novel receptor ligand can be expressed in
XX      transformed host cells and used in methods for regulating the
XX      development, maintenance or regeneration of different cells (e.g.
XX      neurons) and tissues in vivo and in vitro. Soluble NLERK2 peptides can be
XX      used to treat injury, disease or abnormality in the nervous system, and
XX      membrane-bound NLERK2 to modulate proliferation, different or survival
XX      e.g. in grafting procedures or transplantation. NLERK2 can also be used
XX      to raise antibodies for use in immunotherapy, and to detect anti-NLERK2
XX      antibodies that may occur in some autoimmune diseases

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XX      SQ      Sequence 340 AA;
XX      Query Match      100.0%; Score 1850; DB 2; Length 340;
XX      Best Local Similarity 100.0%; Pred. No. 2.5e-142;
XX      Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1 MCPPHSGPGGVAVGALLLGLVGLVSGLSLPEPYMNSANKRFQAEQGYLYLPQIGDRLL 60
Db      1 MCPPHSGPGGVAVGALLLGLVGLVSGLSLPEPYMNSANKRFQAEQGYLYLPQIGDRLL 60
Qy      61 LCPRARPPGHSSPNYEFKYLIVGAGRCRCAPAPNLLITCDRDLDAFTIKFQRY 120
Db      61 LCPRARPPGHSSPNYEFKYLIVGAGRCRCAPAPNLLITCDRDLDAFTIKFQRY 120
Qy      121 SPMLWGHFRSHHDYIITISDGTREGLESLOGGVCLTQGMKYLAVGQSPRGCAVPRKP 180
Db      121 SPMLWGHFRSHHDYIITISDGTREGLESLOGGVCLTQGMKYLAVGQSPRGCAVPRKP 180
Qy      181 VSEMPERDRGAHSLPEKENVLPDPTSNATSRGAEGLPPPSMPAVAVGAAGLALLLL 240
Db      181 VSEMPERDRGAHSLPEKENVLPDPTSNATSRGAEGLPPPSMPAVAVGAAGLALLLL 240
Qy      241 GVAAGAGAMCWMRRRAKPSRSSHPGSGFGRGSLGLGGGGMGPREAPPELGIALRG 300
Db      241 GVAAGAGAMCWMRRRAKPSRSSHPGSGFGRGSLGLGGGGMGPREAPPELGIALRG 300
Qy      301 GAADPPFCPHYEKVSGDYGHPIYIVODGPPQSPPNITYYKV 340
Db      301 GAADPPFCPHYEKVSGDYGHPIYIVODGPPQSPPNITYYKV 340

RESULT 4
ABU07845
ID      ABU07845 standard; protein; 340 AA.
XX      ABU07845;
XX      10-MAY-2003 (first entry)
XX      Human ephrin-B3 ligand.
XX      Cytostatic; vasodilator; antiinflammatory; cardiact; gene therapy;
XX      KW ligand-receptor binding modulator; ephrin ligand; angiogenesis;
XX      lymphangiogenesis; aberrant Ephrin-Tie biology; cell growth disorder;
XX      cell migration disorder; cell proliferation disorder; neovascularisation;
XX      ischaemia; infarction; tissue graft; transplant; human; ephrin-B3;
XX      tie receptor tyrosine kinase; Eph receptor ligand.
XX      Homo sapiens.
XX      WO2003004529-A2.
XX      16-JAN-2003.
XX      02-JUL-2002; 2002WC-1B002524.
XX      02-JUL-2001; 2001US-0302960P.
XX      (LICN ) LICENTIA LTD.
XX      Alitalo K, Kubo H;
XX      WPI; 2003-210341/20.
XX      N-PSDB; ABX12546.
XX      Identifying modulators of binding between a Tie receptor tyrosine kinase
XX      and an Ephrin ligand, useful for promoting neovascularization, comprises
XX      contacting a Tie receptor with an Ephrin in the presence of a putative
XX      modulator.
XX      Disclosure; Page 117-119; 199pp; English.

```

CC The invention describes a method of identifying a modulator of binding
CC between a Tie receptor tyrosine kinase and an Ephrin ligand. The method
CC comprises contacting a Tie receptor composition with an Ephrin
CC composition in the presence and in the absence of a putative modulator
CC compound, and detecting the binding between the Tie receptor and the Ephrin
CC in the presence and in the absence of the putative modulator. The method
CC is useful for identifying a modulator of binding between a Tie receptor
CC tyrosine kinase and an Ephrin ligand. Modulators identified from the
CC method are useful in modulating angiogenic processes, including
CC lymphangiogenesis, for treating diseases associated with aberrant Ephrin-
CC Tie biology, aberrant growth, migration or proliferation of cells that
CC express a Tie receptor, or for promoting growth of vessel or
CC neovascularisation (e.g. ischaemic tissue, an infarction, a new or
CC chronic compound, or a tissue graft or transplant). This is the amino
CC acid sequence of human Ephrin-B3, a member of the Ephrin-B subclass of
CC ligands that are bound to the membrane via a transmembrane domain and
CC short cytoplasmic tail and function as Eph receptor ligands

XX Sequence 340 AA;

SQ Query Match 100.0%; Score 1850; DB 6; Length 340;

Best Local Similarity 100.0%; Pred. No. 2.5e-142;

Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGPPHSGPGGVAVGALLLGLVGLVSGLSLEPVYVNSANKRFOAGGYVLYPOIGRDL 60
DB 1 MGPPHSGPGGVAVGALLLGLVGLVSGLSLEPVYVNSANKRFOAGGYVLYPOIGRDL 60
QY 61 LCPRARPPGHSSPNVEFYKLYLVGAQGRCEAPAPMLLTCDPDDDLFTTKFOEY 120
DB 61 LCPRARPPGHSSPNVEFYKLYLVGAQGRCEAPAPMLLTCDPDDDLFTTKFOEY 120
QY 121 SPNLWGEHFRSHHDYIITSDGTREGLSLOGGVCLTRGMKVLLRVGSPRGAVPRKP 180
DB 121 SPNLWGEHFRSHHDYIITSDGTREGLSLOGGVCLTRGMKVLLRVGSPRGAVPRKP 180
QY 181 VSEMPERDRGAHSLPEKKNLPDPTSNATSRGABGLPPSPMPAVAGAGGLALLL 240
DB 181 VSEMPERDRGAHSLPEKKNLPDPTSNATSRGABGLPPSPMPAVAGAGGLALLL 240
QY 241 GVAAGAGAMCWRRRRAKPSERHPGSGFRGGSGLGGGGGMGPREAPGELGIALRG 300
DB 241 GVAAGAGAMCWRRRRAKPSERHPGSGFRGGSGLGGGGGMGPREAPGELGIALRG 300
QY 301 GAADPPFCPHYEKVSGDYGHPIYIVODGPPQSPPIIYKYV 340
DB 301 GAADPPFCPHYEKVSGDYGHPIYIVODGPPQSPPIIYKYV 340

RESULT 5
ADQ21436 standard; protein; 340 AA.

XX ID ADQ21436 standard; protein; 340 AA.

XX AC ADQ21436;

XX DT 26-AUG-2004 (first entry)

XX DE Human soft tissue sarcoma-upregulated protein - SEQ ID 4256.

XX KW soft tissue sarcoma; cytoskeletal; gene therapy; vaccine; screening; human.

XX OS Homo sapiens.

XX PN WO2004048938-A2.

XX PD 10-JUN-2004.

XX PF 26-NOV-2003; 2003WO-US038193.

XX PR 26-NOV-2002; 2002US-0429739P.

XX PA (PROT-) PROTEIN DESIGN LABS INC.

PI Aziz N, Ginsburg WM, Zlocznik A;
XX WPI; 2004-441208/41.
XX Early detection of soft tissue sarcoma comprises determining expression
PT of a gene in a first soft tissue sample and a normal soft tissue sample
PT and comparing the gene expression, also useful in treating soft tissue
XX sarcoma.
PS Example 2; SEQ ID NO 4256; 210bp; English.

XX The invention relates to a novel method for detecting soft tissue sarcoma
CC which comprises obtaining a first soft tissue sample from an individual
CC and a normal soft tissue sample from the same or different individual,
CC determining the expression of a gene in both samples and comparing the
CC expression of the gene in both soft tissue samples, where a higher level
CC of protein expression in the first soft tissue sample indicates the
CC presence of soft tissue sarcoma. The method of the invention has
CC cytoskeletal applications and may be useful for detecting soft tissue
CC sarcoma, possibly via gene therapy or vaccine production. The nucleic
CC acid sequences may be useful in diagnostic and screening applications.
CC The current sequence is that of a human soft tissue sarcoma-upregulated
CC protein of the invention. The current sequence is not shown within the
CC specification per se but was submitted in CD format by the inventor.

XX Sequence 340 AA;

SQ Query Match 100.0%; Score 1850; DB 8; Length 340;

Best Local Similarity 100.0%; Pred. No. 2.5e-142;

Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGPPHSGPGGVAVGALLLGLVGLVSGLSLEPVYVNSANKRFOAGGYVLYPOIGRDL 60
DB 1 MGPPHSGPGGVAVGALLLGLVGLVSGLSLEPVYVNSANKRFOAGGYVLYPOIGRDL 60
QY 61 LCPRARPPGHSSPNVEFYKLYLVGAQGRCEAPAPMLLTCDPDDDLFTTKFOEY 120
DB 61 LCPRARPPGHSSPNVEFYKLYLVGAQGRCEAPAPMLLTCDPDDDLFTTKFOEY 120
QY 121 SPNLWGEHFRSHHDYIITSDGTREGLSLOGGVCLTRGMKVLLRVGSPRGAVPRKP 180
DB 121 SPNLWGEHFRSHHDYIITSDGTREGLSLOGGVCLTRGMKVLLRVGSPRGAVPRKP 180
QY 181 VSEMPERDRGAHSLPEKKNLPDPTSNATSRGABGLPPSPMPAVAGAGGLALLL 240
DB 181 VSEMPERDRGAHSLPEKKNLPDPTSNATSRGABGLPPSPMPAVAGAGGLALLL 240
QY 241 GVAAGAGAMCWRRRRAKPSERHPGSGFRGGSGLGGGGGMGPREAPGELGIALRG 300
DB 241 GVAAGAGAMCWRRRRAKPSERHPGSGFRGGSGLGGGGGMGPREAPGELGIALRG 300
QY 301 GAADPPFCPHYEKVSGDYGHPIYIVODGPPQSPPIIYKYV 340
DB 301 GAADPPFCPHYEKVSGDYGHPIYIVODGPPQSPPIIYKYV 340

RESULT 6
ADVS1247 standard; protein; 340 AA.

XX ID ADVS1247 standard; protein; 340 AA.

XX AC ADVS1247;

XX DT 19-MAY-2005 (first entry)

XX DE Human ephrin-B3 SEQ ID NO:16.

XX KW ephrin; hematopoiesis; hyperproliferation; cytoskeletal; anti-neoplastic;
XX anti-inflammatory; antiproliferative; gastrointestinal-gen.; dermatological;
XX coagulant; immunostimulant; cerebroprotective; vasotropic; antitumor.

XX OS Homo sapiens.

XX PN US2005049194-A1.

```

XX 03-MAR-2005.
PD
XX
XX 31-OCT-2003; 2003US-00698907.
PR
XX 09-NOV-2001; 2001US-0345206P.
XX 02-JUL-2002; 2002US-0393722P.
PR 08-NOV-2002; 2002US-00291290.
PR 03-APR-2003; 2003US-0460488P.
XX
PA (FRIS/) FRISEN J.
PA (HOLM/) HOLMBERG J.
XX
PI Frisen J, Holmberg J;
XX WPI; 2005-195317/20.
DR
XX Use of ephrin and its molecules for alleviating a symptom or a disorder
PT with reduced levels of hematopoiesis, increased levels of cellular
PT proliferation in an intestinal tract, or abnormal level of cellular
PT proliferation in a tissue.
XX
PS Disclosure; SEQ ID NO 16; 68bp; English.
XX
XX The invention relates to a novel use of ephrin, ephrin inhibitors, and
XX ephrin receptors for alleviating a symptom of a disorder having reduced
XX levels of hematopoiesis, having increased levels of cellular
XX proliferation in an intestinal tract, or having an abnormal level of
XX cellular proliferation in a tissue. A composition of the invention has
XX cytostatic, antiangiogenic, antiinflammatory, gastrointestinal
XX -gen., dermatological, coagulant, immunostimulant, cerebroprotective,
XX vasoconstrictive, and antitumor activity. The present sequence represents
XX murine ephrin-B3.
XX
SQ Sequence 340 AA;
Query Match 100.0%; Score 1850; DB 9; Length 340;
Best Local Similarity 100.0%; Pred. No. 2,5e-142;
Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGPBHSFGGVVGVALLLGLVGLVSGLSLEPYMNSANKRFQAEQGYLYPQIGRLDL 60
DB 1 MGPBHSFGGVVGVALLLGLVGLVSGLSLEPYMNSANKRFQAEQGYLYPQIGRLDL 60
QY 61 LCPRARPPGPHSSPNTEFYKLYLVGAQGRCEAPAPMLLLTCDBPDLRLFTTFQRY 120
DB 61 LCPRARPPGPHSSPNTEFYKLYLVGAQGRCEAPAPMLLLTCDBPDLRLFTTFQRY 120
QY 121 SPNLMGHERSHHDYIIATSDGTREGESLQGVCLTRGMKVLRLVGQSPRGAVPRKP 180
DB 121 SPNLMGHERSHHDYIIATSDGTREGESLQGVCLTRGMKVLRLVGQSPRGAVPRKP 180
QY 181 VSEMPMERDRGAHSLPEGKENVLPDPTSNATSRGAEGLPPSPMPAVAGAAGLALLL 240
DB 181 VSEMPMERDRGAHSLPEGKENVLPDPTSNATSRGAEGLPPSPMPAVAGAAGLALLL 240
QY 241 GVAAGAGAMCWRRRRAKPSRRPGSGFGRGSLGLGGGGGMPREAEPEGIGIALRG 300
DB 241 GVAAGAGAMCWRRRRAKPSRRPGSGFGRGSLGLGGGGGMPREAEPEGIGIALRG 300
QY 301 GAADPPCCPHYEKVSGDYGHVYIYODGPPQSPNIIYKV 340
DB 301 GAADPPCCPHYEKVSGDYGHVYIYODGPPQSPNIIYKV 340

```

```

DE Eph family ligand Efl-6.
XX
XX Efl-6; Eph; Etk; receptor tyrosine kinase; signal transduction; ligand;
XX neurological disease.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 1..24
XX /label= Sig_peptide
XX Protein 25..340
XX /label= Mat_protein
XX Misc-difference 166
XX /label= Gln, Arg
XX Domain 225..249
XX /label= Transmembrane_domain
XX
XX WO9715667-A1.
XX 01-MAY-1997.
XX
XX 25-OCT-1996; 96WO-US017201.
XX
XX 25-OCT-1995; 95US-0007015P.
XX
XX (REG- ) REGENERON PHARM INC.
XX
XX Davis S, Gale NW, Yancopoulos GD;
XX WPI; 1997-259021/23.
XX N-PSDB; AAT69808.
XX
XX New nucleic acid encoding Efl-6 ligand protein - used for promoting
XX growth and proliferation of neuronal cells and in drug screening.
XX
XX Claim 2; Fig 1; 36pp; English.
XX
XX A novel ligand (AAM17081), designated Efl-6 (or Eph transmembrane
XX tyrosine kinase family ligand 6), binds to the Etk, Ntk/Cek5, Hek2/Sek4,
XX Htk and Sek1 receptors on cells. Its amino acid sequence was deduced from
XX a human frontal cortex cDNA clone (AAT69808). Recombinant Efl-6,
XX truncated soluble polypeptides comprising the extracellular domain of Efl-
XX -6, and Efl-6 ligand-bodies comprising soluble Efl-6 and the Fc portion of
XX IgG, can be expressed in host cells. These can be used to support neuronal
XX and other Eph receptor-bearing cell populations for treatment of
XX neurological disorders, in drug screening and to raise diagnostic
XX antibodies
XX
SQ Sequence 340 AA;
Query Match 99.7%; Score 1844; DB 2; Length 340;
Best Local Similarity 99.7%; Pred. No. 7,8e-142;
Matches 339; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MGPBHSFGGVVGVALLLGLVGLVSGLSLEPYMNSANKRFQAEQGYLYPQIGRLDL 60
DB 1 MGPBHSFGGVVGVALLLGLVGLVSGLSLEPYMNSANKRFQAEQGYLYPQIGRLDL 60
QY 61 LCPRARPPGPHSSPNTEFYKLYLVGAQGRCEAPAPMLLLTCDBPDLRLFTTFQRY 120
DB 61 LCPRARPPGPHSSPNTEFYKLYLVGAQGRCEAPAPMLLLTCDBPDLRLFTTFQRY 120
QY 121 SPNLMGHERSHHDYIIATSDGTREGESLQGVCLTRGMKVLRLVGQSPRGAVPRKP 180
DB 121 SPNLMGHERSHHDYIIATSDGTREGESLQGVCLTRGMKVLRLVGQSPRGAVPRKP 180
QY 181 VSEMPMERDRGAHSLPEGKENVLPDPTSNATSRGAEGLPPSPMPAVAGAAGLALLL 240
DB 181 VSEMPMERDRGAHSLPEGKENVLPDPTSNATSRGAEGLPPSPMPAVAGAAGLALLL 240
QY 241 GVAAGAGAMCWRRRRAKPSRRPGSGFGRGSLGLGGGGGMPREAEPEGIGIALRG 300
DB 241 GVAAGAGAMCWRRRRAKPSRRPGSGFGRGSLGLGGGGGMPREAEPEGIGIALRG 300

```

QY 301 GAADPPFCPHYEKVSGDYGHPIYIVODGPPQSPNNIYY 340
 DB 301 GAADPPFCPHYEKVSGDYGHPIYIVODGPPQSPNNIYY 340

RESULT 8

AAW33698 standard; protein; 455 AA.

AAW33698;

30-APR-1998 (first entry)

AL-2-long (AL-21) protein.

AL-21; AL-2-long; human; treatment; neurological disorder; tumour;

rheumatoid arthritis; wound healing; paralysis; angiogenesis; leukaemia;

psoriasis; Alzheimer's disease; epilepsy.

Homo sapiens.

Key Location/Qualifiers

Peptide 1..26 /note="signal peptide"

Protein 27..455 /note="mature protein"

Domain 27..219 /note="extracellular domain"

Domain 220..245 /note="hydrophobic transmembrane domain"

MO9740153-AL.

30-OCT-1997.

17-APR-1997; 97WO-US006345.

19-APR-1996; 96US-00635130.

(GETH) GENENTECH INC.

Caras IW;

WPI; 1997-535837/49.

N-PSDB; AAV06354.

Human AL-2 neurotrophic factor and related DNA - used to develop products for, e.g. treating neurologic disorders, angiogenesis disorders, tumours or rheumatoid arthritis or for wound healing.

Claim 20; Fig 1A-C; 86pp; English.

This is a AL-2-long (AL-21) protein. The AL-2 is a novel Eph-related tyrosine kinase receptor ligand. AL-2 can be administered to patients in whom the nervous system has been damaged by trauma, surgery, stroke, ischaemia, infection, metabolic disease, nutritional deficiency, malignancy, or toxic agents, to promote the survival or growth of neurons. They can be used to treat mononeuron disorders such as amyotrophic lateral sclerosis (Lou Gehrig's disease), Bell's palsy, and various conditions involving spinal muscular atrophy, or paralysis. AL-2 can be used to treat human neurodegenerative disorders, such as Alzheimer's disease, Parkinson's disease, epilepsy, demyelinating diseases such as multiple sclerosis, Huntingtons chorea, Down's syndrome, nerve deafness, Menier's disease, and other disorders of the cerebellum. AL-2 can be used as cognitive enhancer, to enhance learning particularly in dementias or trauma, since they can promote axonal outgrowth and synaptic plasticity, particularly of hippocampal neurons that express AL-2 binding Eph-family receptors and cortical neurons that express AL-2. AL-2 can also be used for wound healing, i.e. accelerating neovascularisation of, e.g. burns and ulcers. The encoding nucleic acids are useful in preparing antibodies that specifically bind to the AL-2 protein. The antibodies and the AL-2 antagonists are useful in diagnosing

CC and treating various neuronal disorders. AL-2 antagonists can be used for CC modulating angiogenesis. They can also be used for the treatment of CC tumours, acute myeloid leukaemia (AML), chronic myeloid leukaemia (CML), CC myelodysplastic syndrome (MDS), diabetic retinopathy, neovascular CC glaucoma, psoriasis and rheumatoid arthritis

Sequence 455 AA;

Query Match 99.5%; Score 1841; DB 2; Length 455;
 Best Local Similarity 100.0%; Pred. No. 1.9e-141;
 Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGPPHSGPGVAVGALLLIGVTLGVSGLSLEPVYNNNSANKRQAGGYLYPQIGRDL 60

DB 1 MGPPHSGPGVAVGALLLIGVTLGVSGLSLEPVYNNNSANKRQAGGYLYPQIGRDL 60

QY 61 LCPRARPPGHSSPYVEFYKLYVGAGQGRCEAPAPYLTLTCRPPDLFTTIKFOY 120

DB 61 LCPRARPPGHSSPYVEFYKLYVGAGQGRCEAPAPYLTLTCRPPDLFTTIKFOY 120

QY 121 SPNLWGHFRSHHDYIIATSDGTREGLESLOGVCLTRGMKVLRLVGQSPRGAVPRKP 180

DB 121 SPNLWGHFRSHHDYIIATSDGTREGLESLOGVCLTRGMKVLRLVGQSPRGAVPRKP 180

QY 181 VSEMERDRGAHSLERKENTLPDPTSNATSRGAEPLPPSPAPVAGAGLALLL 240

DB 181 VSEMERDRGAHSLERKENTLPDPTSNATSRGAEPLPPSPAPVAGAGLALLL 240

QY 241 GYAGAGGACWRRRAKPSERHPGPGSFGRGSLGLGGGGMGPAREPGEIGTALRG 300

DB 241 GYAGAGGACWRRRAKPSERHPGPGSFGRGSLGLGGGGMGPAREPGEIGTALRG 300

QY 301 GAADPPFCPHYEKVSGDYGHPIYIVODGPPQSPNNIYY 338

DB 301 GAADPPFCPHYEKVSGDYGHPIYIVODGPPQSPNNIYY 338

RESULT 9

AAW46615

ID AAW46615 standard; protein; 340 AA.

AAW46615;

06-JUL-1998 (first entry)

Human transmembrane ligand Elk-L3.

Elk-L3; Elk-related receptor tyrosine kinase; transmembrane ligand;

human; signal transduction; axonogenesis; nerve cell; neurone;

Alzheimer's disease; Parkinson's disease; Huntingdon's disease;

demyelination; multiple sclerosis; amyotrophic lateral sclerosis;

neurological polynuropathy; progressive supranuclear palsy;

Shy Drager's syndrome; multistem degeneration;

olivo ponto cerebellar atrophy; peripheral nerve damage.

Homo sapiens.

Key

Misc-difference 166 Location/Qualifiers

FT Domain //label=Gln, Arg 225..249

PN MO9801548-AL.

PD 15-JAN-1998.

PF 04-JUL-1997; 97WO-CA000473.

PR 05-JUL-1996; 96US-0021272P.

PA (MOON) MOUNT SINAI HOSPITAL CORP.

XX Holland S, Mbamalu G, Pawson T;
 XX WPI, 1998-101047/09.
 XX N-PSDB; AAV16097.
 DR
 XX
 XX Modulating transmembrane ligand for an Elk-related receptor tyrosine kinase - by formation of a complex between an oligomerised Elk-related receptor tyrosine kinase and a transmembrane ligand.
 XX
 XX
 PS Disclosure, Fig 5A; 40pp; English.

This polypeptide comprises human ELK-13, a transmembrane ligand of ELK-related receptor tyrosine kinase (ERRK). A novel method of modulating the biological activity of, or for affecting a pathway regulated by, a transmembrane ligand for an ERRK in a cell expressing the transmembrane ligand comprises forming a complex between a purified and isolated oligomerised ERRK, or an isoform or an extracellular domain of the ERRK, and the transmembrane ligand expressed on the cell. The complex can also be used for evaluating a substance for its ability to modulate the biological activity of a transmembrane ligand for an ERRK, and to identify substances that affect or modulate a pathway regulated by a ERRK. A purified and isolated oligomerised ERRK can be used in the preparation of a medicament for modulating neuronal development or regeneration in a subject, or in a medicament for modulating axonogenesis in a subject (all claimed). The substances identified by the methods can be used to modulate axonogenesis, nerve cell interactions and regeneration, to treat diseases and conditions involving trauma and injury to the nervous system, such as Alzheimer's disease, Parkinson's disease, Huntington's disease, demyelinating diseases, such as multiple sclerosis, amyotrophic lateral sclerosis, bacterial and viral infections of the nervous system, deficiency diseases, such as Wernicke's disease and nutritional polyneuropathy, progressive supranuclear palsy, Shy Drager's syndrome, multistep degeneration and olivoponto cerebellar atrophy, peripheral nerve damage, trauma, and ischaemia resulting from stroke

Sequence 340 AA;

Query match	99.2%	Score 1836	DB 2	Length 340
-------------	-------	------------	------	------------

Best local Similarity 99.4%; Pred. No. 3.5e-141;
Matches 338; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Matches 338; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	1	MGPHSGPGGVIRGALLLLGVLGVLGSLSELEVYNNANKFQAEQGVYLPQIGDLDL	60
Db	1	MGPHSGPGGVIRGALLLLGVLGVLGSLSELEVYNNANKFQAEQGVYLPQIGDRLD	60
QY	61	LCRRARPPOGHSSPNEFYKLYLVGGAQRCEAPAPRLLLTCDRPRDLRFITKQEY	120
Db	61	LCRRARPPOGHSSPNEFYKLYLVGGAQRCEAPAPRLLLTCDRPRDLRFITKQEY	120
QY	121	SPPLMHGHEFRSHHDYIIATSDGTREGLESLQGGVCLTRGMKVLRLVQSGPRGAVPRKP	180
Db	121	SPPLMHGHEFRSHHDYIIATSDGTREGLESLQGGVCLTRGMKVLRLXVQSGPRGAVPRKP	180
QY	181	VSEMPMERDRGAHSLSEPGKENLPEDPTSNATSRGAEGLPPSPVAVAGAGLALLL	240
Db	181	VSEMPMERDRGAHSLSEPGKENLPEDPTSNATSRGAEGLPPSPVAVAGAGLALLL	240
QY	241	GVAGAGGAMCWRRAKPSERHPPGGSFGRGSGSLGCGGGMGPREAPBELITALRG	300
Db	241	GVAGAGGAMCWRRAKPSERHPPGGSFGRGSGSLGCGGGMGPREAPBELITALRG	300
QY	301	GAADPPCCPHYEKVSGDYGHPYIYVDGPPQSPNNIYKV	340
Db	301	GAADPPCCPHYEKVSGDYGHPYIYVDGPPQSPNNIYKV	340

RESULT 10	
ABU07846	
ID	ABU07846 standard; protein; 340 AA
XX	
AC	ABU07846;

XX	
DT	10-MAY-2003 (first entry)
XX	
DE	Mouse ephrin-B3 ligand.
XX	
KM	Cytostatic; vasodilator; antiinflammatory; cardiac; gene therapy;
KM	ligand-receptor binding modulator; ephrin ligand; angiogenesis;
KM	lymphangiogenesis; aberrant Ephrin-Tie biology; cell growth disorder;
KM	cell migration disorder; cell proliferation disorder; neovascularisation.
KM	ischaemia; infarction; tissue graft; transplant; mouse; ephrin-B3;
KM	the receptor tyrosine kinase; Eph receptor ligand.

Mus musculus.

PN WO2003004529-A2.

PD 16-JAN-2003

PF 02-JUL-2002; 2002WO-IB002524.

PR 02-JUL-2001; 2001US-0302960P.

PA (LICN) LICENTIA LTD.

PI Alitalo K, Kubo H;

DR WPI; 2003-210341/20

22X

PT Identifying modulators of binding between a Tie receptor tyrosine kinase
PT and an Ephrin ligand, useful for promoting neovascularization, comprises
PT contacting a Tie receptor with an Ephrin in the presence of a putative
PT modulator.

PS Disclosure; Page 121-122; 199pp; English.

CC The invention describes a method of identifying a modulator of binding
CC between a Tie receptor tyrosine kinase and an Ephrin ligand. The method
CC comprises contacting a Tie receptor composition with an Ephrin
CC composition in the presence and in the absence of a putative modulator
CC compound, and detecting the binding between Tie receptor and the Ephrin
CC in the presence and in the absence of the putative modulator. The method
CC is useful for identifying a modulator of binding between a Tie receptor
CC tyrosine kinase and an Ephrin ligand. Modulators identified from the
CC method are useful in modulating angiogenic processes, including
CC lymphangiogenesis, for treating diseases associated with aberrant Ephrin
CC Tie biology, aberrant growth, migration or proliferation of cells that
CC express a Tie receptor, or for promoting growth of vessel or
CC neovascularisation (e.g. ischaemic tissue, an infarction, a new or
CC chronic compound, or a tissue graft or transplant). This is the amino
CC acid sequence of mouse Ephrin-B3, a member of the Ephrin-B subclass of
CC ligands that are bound to the membrane via a transmembrane domain and
CC short cytoplasmic tail and function as Eph receptor ligands

SQ Sequence 340 AA;

Query Match 96.2%; Score 1780; DB 6; Length 340;

Best Local Similarity 95.6%; Pred. No. 1.3e-136;
Matches 325; Conservative 7; Mismatches 8; Indels 0; Gaps 0.

Matches 325; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

[illegible]

Db	181	VSMPEPRDRGAHNSLEPGDITLPGDPSSNATSRKAEGELPPSPMPAVAGAGSMALLL	240
QY	241	GVAGAGAMCWRRRRAKPSBSRHPGSPGSGSLGAGGGGAMGPBEALPGELIALRG	300
Db	241	GVAGAGAMCWRRRRAKPSBSRHPGSPGSGSLGAGGGGAMGPBEALPGELIALRG	300
QY	301	GAADPFCPHYKESGDYHPVYIYODGPGSPPIIYKV	340
Db	301	GTADPFCPHYKESGDYHPVYIYODGPGSPPIIYKV	340

```

RESULT 11
ADY51239
ID ADY51239 standard; protein; 340 AA.
XX
AC ADY51239;
XX
DT 19-MAY-2005 (first entry)
XX
DE Mouse ephrin-B3 SEQ ID NO:8.
XX

```

KM ephrin; hematopoiesis; hyperproliferation; cytosolic; antiapoptotic;
KM antiinflammatory; antiproliferative; gastrointestinal-gen.; dermatological
KM coagulant; immunostimulant; cerebroprotective; vasotropic; antitumor.
XX
XX
OS *Mus musculus*.
XX
XX
PN US2005049194-A1.
XX
XX
PD 03-MAR-2005.
XX
XX
31-OCT-2003; 2003US-00698907.
PF
XX
XX
09-NOV-2001; 2001US-0345206P.
PR
02-JUL-2002; 2002US-0393272P.
PR
08-NOV-2002; 2002US-00291290.
PR
03-APR-2003; 2003US-0460488P.
PR

PA (FRIS/) FRISEN J.
PA (HOLM/) HOLMBERG J.
XX
XX
PI Friesen J, Holmberg J;
XX
XX
DR WPI, 2005-195317/20.
XX
XX
XX Use of ephrin and its molecules for alleviating a symptom or a disorder
PT with reduced levels of hematopoiesis, increased levels of cellular
PT proliferation in an intestinal tract, or abnormal level of cellular
PT proliferation in a tissue.

XX The invention relates to a novel use of ephrin, ephrin inhibitors, and
XX ephrin receptors for alleviating a symptom of a disorder having reduced
CC levels of hematopoiesis, having increased levels of cellular
CC proliferation in an intestinal tract, or having an abnormal level of
CC cellular proliferation in a tissue. A composition of the invention has
CC cytosstatic, antiamebic, antiinflammatory, antiparasitic, gastrointestinal
CC -gen., dermatological, coagulant, immunostimulant, cerebroprotective,
CC vasotropic, and antitumor activity. The present sequence represents
CC murine ephrin-B3.
XX
XX Sequence 340 AA;
XQ
PS Disclosure; SEQ ID NO 8; 68bp; English.

Query Match	96.2%	Score 1780;	DB 9;	Length 340;
Best Local Similarly	95.6%	Pred. No. 1.3e-136;		
Matches 325; Conservative	7;	Mismatches 8;	Indels 0;	Gaps 0;

Oy		I MGP RHSGPGGVRV GALLILGLVLVS GSLEPVTWNSANKR FQAEGGYLTYPQIGRDLDL 600
Dd		I MGAPRHSGPGGV R V GALLILLGFAGTIVS GSLESPVTWN SANKRFQAEGGYLTYPQIGRDLDL 600

Qy	61	LCGRAPRPPHSSPNVEFEKYLVLGGACGRCSEAPRANLLITCDRBDLLRFITKQEX	120
Db	61	LCRRAPRPPHSSPSSEFEKYLVLGGAQGRCEAPRANLLITCDRBDLLRFITKQEX	120
Qy	121	SPPLMGHERSHHDYIIATSDGTREGLESLOGGVCILRGKULLRRQSGPRGSAVERKP	180
Db	121	SPPLMGHERSHHDYIIATSDGTREGLESLOGGVCILRGKULLRRQSGPRGSAVERKP	180
Qy	181	VSEMPHERPRGAHSLSEPKENTLPCDPRFSNNLTSGAGRPRLPRSPMPVAGAAGTALLLL	240
Db	181	VSEMPHERPRGAHSLSEPKRDTLPEDPSNNLTSGAKSEPLRPRSPMPVAGAAGTALLLL	240
Qy	241	GVAGAGAGACMRRRAKDSERKHPGSGFGKSGISLIGGGGGMGRREARPEGELIALRG	300
Db	241	GVAGAGAGACMRRRRRAKDSERHHPGSGFGKSGISLIGGGGGMGRREARPEGELIALRG	300
Qy	301	GAADPRFCSEHYKVGSDGHPYIYLQDDPRPOSPPRIITYKV	340
Db	301	GTADPRFCSEHYKVGSDGHPYIYLQDDPRPOSPPRIITYKV	340

RESULT 12
ADJ70889
ID ADJ70889 standard; protein; 285 AA

AC ADJ70889;

DT 06-MAY-2004 (first entry)

DE Human heat mitochondrial protein as a therapeutic target SeqID2695.

KM mitochondrial; human; screening assay; diabetes mellitus;
 KM Huntington's disease; osteoarthritis;
 KM Leber's hereditary optic neuropathy; LHON;
 KM mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
 KM myoclonal epilepsy ragged red fibre syndrome; MERRF; cancer;
 KM neuroprotective; neurotropic; antidiabetic; anticonvulsant; antiarthritic;
 KM osteopathic; ophthalmological; cytostatic.

OS Homo sapiens

PN WO2003087768-A2.

PD 23-OCT-2003.

PF 04-APR-2003; 2003WO-US010870.

PR 12-APR-2002; 2002US-0372843P.

PR 20-SEP-2002; 2002US-0412418P.

PA (MITO-) MITOKOR.

XX

PI Warrnack DE;

DR WPI; 2003-845369/78.

PT Identifying a mitochondrial target for drug screening assays and for
PT treating diseases associated with altered mitochondrial function,
PT comprises detecting a modified polypeptide in a sample and correlating
PT with the disease.

PS Claim 1; SEQ ID NO 2695; 180bp; English

CC This invention relates to novel mitochondrial targets that can be used
CC for therapeutic intervention in treating a disease associated with
CC altered mitochondrial function. Specifically, it refers to a method for
CC identifying proteins of the human heart mitochondrial proteome that are
CC useful for drug screening assays, as well as therapeutic targets. The
CC present invention describes a method for identifying such proteins that
CC can be used in the treatment of various diseases associated with altered

CC mitochondrial function including diabetes mellitus, Huntington's disease,
 CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
 CC encephalopathy, lactic acidosis and stroke (MELAS), myoclonic epilepsy
 CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
 CC compositions have neuroprotective, nootropic, antidiabetic,
 CC anticonvulsant, anticholinergic, osteopathic, ophthalmological and
 CC cytostatic activities. This polypeptide sequence is a human heart
 CC mitochondrial protein of the invention.

XX Sequence 285 AA;

QY Query Match 84.3%; Score 1559; DB 7; Length 285;
 Best Local Similarity 100.0%; Pred. No. 1.1e-118;
 Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 DRDLDCPRARPPGPHSSPVEFYKYLVGAGRCRCAPPAVNLITCDRPLDLRFTI 115
 |||
 QY 116 KFOEYSPLMGHFRSHHDYIATSDGTRGLESLOGGVCLTRGKVLRLVGQSPRGGA 175
 61 KFOEYSPLMGHFRSHHDYIATSDGTRGLESLOGGVCLTRGKVLRLVGQSPRGGA 120
 |||
 DB 121 VPRKPVSEMPMERDRGAHSLRPGKENTLPDPTSNATSRGAEGLRPPSPMAVAGAAGL 180
 |||
 QY 176 VPRKPVSEMPMERDRGAHSLRPGKENTLPDPTSNATSRGAEGLRPPSPMAVAGAAGL 235
 |||
 DB 121 VPRKPVSEMPMERDRGAHSLRPGKENTLPDPTSNATSRGAEGLRPPSPMAVAGAAGL 180
 |||
 QY 236 ALLLGVAGAGCMCRRRRRAKPSRSRHPGSGFSGGSLGCGGGGMPREAPBELGI 295
 181 ALLLGVAGAGCMCRRRRRAKPSRSRHPGSGFSGGSLGCGGGGMPREAPBELGI 240
 |||
 DB 296 ALRGGGADPPFCPHYKVSQDYGHPYIYQDGPPOSPPIYKYV 340
 241 ALRGGGADPPFCPHYKVSQDYGHPYIYQDGPPOSPPIYKYV 285
 |||

RESULT 13
 ID AAM00287 standard; protein; 334 AA.
 AC AAM00287;
 XX
 XX 19-JAN-1997 (first entry)
 DT
 XX
 XX Mouse Bph receptor ligand ELF-2.
 DE
 KW Bph receptor; ligand; ELF-2; tyrosine kinase; signal transduction;
 KW organogenesis; oncogenesis; tumour; neurological disorder; diagnosis;
 KW gene therapy.
 XX
 XX Mus sp.
 OS
 XX
 XX Key Location/Qualifiers
 FH Domain 1..224
 FT Binding-site /label= Extracellular_domain
 FT Binding-site 31..155
 FT Domain /label= Receptor_binding_site
 FT Domain 226..251
 FT /label= Transmembrane_domain
 PN WO9626958-A2.
 XX
 XX PD 06-SEP-1996.
 XX
 XX PP 23-FEB-1996; 96WO-US002673.
 XX
 XX PR 27-FEB-1995; 95US-00395415.
 XX
 XX PA (HARD) HARVARD COLLEGE.
 XX
 XX PI Flanagan JG, Bergemann AD;
 XX
 XX DR WPI, 1996-433391/43.

DR N-PSDB; AAT40230.
 XX
 XX Bph receptor ligand, ELF-2, and DNA encoding it : used to treat or
 PT prevent neurological diseases, and to modulate binding of ELF-2 to Bph
 PT receptor, e.g. to prevent or treat tumour formation.
 XX
 XX Claim 6; Fig 1A-B; 50pp; English.
 XX
 CC Mouse Bph receptor ligand ELF-2 (AAM00287) is strongly expressed in the
 CC anterior hindbrain and newly-forming somites of embryos at the early
 CC organogenesis stage of development. It is important in cellular
 CC communication during pattern formation. Its amino acid sequence was
 CC deduced from a cDNA clone (AAT40230) isolated from a newborn mouse brain
 CC cDNA library. The ELF-2 ligand can be used to alter neurological
 CC development, oncogenesis and growth regulation, to modulate binding of
 CC ELF-2 to the Bph receptor, and in diagnostic assays

XX Sequence 334 AA;

QY Query Match 34.5%; Score 637.5; DB 2; Length 334;
 Best Local Similarity 42.1%; Pred. No. 1.8e-43;
 Matches 139; Conservative 49; Mismatches 129; Indels 13; Gaps 5;

DB 14 GALLLGVILVGLSLRPEYWNANKRQAEGYVLPQIGDRDLDCPRARPPGPHSS 73
 15 GLMLVLCRTAISRSIVLEPIYWNSSKFLPGGGLVLYQIGDKLDICKV--DSKTV 71
 |||
 QY 74 PNYEFKYLTVGAGRCRCAPPAVNLITCDRPLDLRFTIYFOEYSPLMGHFRSHH 133
 |||
 DB 72 GQYEVYKVMVWDQADRCTIKKENTPLNCAIPDDVFTTIFQESPLMLGLEFOKNK 131
 |||
 QY 134 DYYIITSDGTRGLESLOGGVCLTRGKVLRLVGQ--SPRGAVRKPSEMPMER-DR 190
 132 DYYIITSDGTRGLESLOGGVCLTRGKVLRLVGQ--SPRGAVRKPSEMPMER-DR 191
 |||
 DB 191 GAHSLRPGKENTLPDPTSNATSRGAEGLRPPSPMAVAGAAGLALLLGVAGAGAMC 250
 192 GRSSTSPFYKPNPGSGSTDSNAGSHGNNLLGSEVALFAGIAGCIIFIIITLVLL 251
 |||
 QY 251 WRRRAKPSRSRHPGSGFSGGSLGCGGGGMPREAPBELGILRGGGAADPPFCRH 310
 |||
 DB 252 KYRRHRKHSPQHTTTLSTLTATPRGGNN---NGSBSPDVIPLR--TDSVFCRH 304
 |||
 QY 311 YEKVSGDYGHPYIYQDGPPOSPPIYKYV 340
 305 YEKVSGDYGHPYIYQDGPPOSPPIYKYV 334
 |||

RESULT 14
 ID AAR92742 standard; protein; 336 AA.
 AC AAR92742;
 XX
 XX 21-MAY-1996 (first entry)
 DT
 XX
 XX Murine hepatoma transmembrane kinase receptor ligand.
 DE
 KW Hepatoma transmembrane kinase; Htk; receptor; ligand; tyrosine kinase;
 KW neurodegenerative disease.
 XX
 XX Mus musculus.
 OS
 XX
 XX PN WO9602645-A2.
 XX
 XX PD 01-FEB-1996.
 XX
 XX PP 14-JUL-1995; 95WO-US008812.
 XX
 XX PR 20-JUL-1994; 94US-00277722.
 XX
 XX PA (GETH) GENENTECH INC.
 XX
 XX DR

PI Bennett BD, Matthews W;
 XX MPI; 1996-105907/11.
 DR N-PSDB; AAT16470.
 XX
 PT Ligand for the hepatoma trans-membrane kinase receptor - useful for
 PT stimulating and inhibiting cells carrying the receptor, e.g. for treating
 PT neuro-degenerative disease.
 XX
 XX Claim 5; Fig 1(A-D); 88pp; English.
 XX
 CC Mouse (AAT16470) and human (AAT16471) Hck ligand which bind to, and
 CC activate, the Hck receptor, have been identified in a variety of tissues
 CC using a soluble Hck-Fc fusion protein. The predicted mol.wt. of the
 CC murine Hck ligand protein following a signal peptide cleavage is 34 kD
 CC with an estimated pI of 8.9. The murine and human ligands show 96%
 CC homology at the amino acid level. The DNA is used to produce recombinant
 CC ligands; for tissue-specific typing (partic. as a marker for breast
 CC cancer) and as a marker for human chromosome 13. The ligands (partic. in
 CC soluble form) are used to activate the tyrosine kinase domain of the Hck
 CC receptor, i.e. to stimulate or inhibit growth, differentiation, and/or
 CC activation of cells contg. the receptor, e.g. treatment of
 CC neurodegenerative diseases, since they are strongly expressed in the
 CC cerebral cortex, hippocampus, striatum and cerebellum. The ligands are
 CC also useful as a control or standard in assays, for generation of
 CC antibodies, as a mol. wt. marker, for growth in vitro of Hck-receptor
 CC positive cells, as research agent, in screening, etc
 XX
 XX Sequence 336 AA;
 SO
 Query Match 34.5%; Score 637.5; DB 2; Length 336;
 Best Local Similarity 42.1%; Pred. No. 1.8e-43;
 Matches 139; Conservative 49; Mismatches 129; Indels 13; Gaps 5;
 QY 14 GALLLLGVLGVSGLSELPYVNSANKRQAEAGGYLVLPQIGDRDLLCPRRAPRPHSS 73
 DB 17 GLMLVLCRTAISRISIVLEPIYWNSSNSKFLPGQGLVLPQIGDKDILCPKV--DSKTV 73
 QY 74 PNYEFKLYLVGAGORCEAPRPAVNLITCDRDLRFTIKFOEYSPNLMGHEFRSHN 133
 DB 74 GQYEVYKVMVDKQADRCTIKKENTPILNCARPDQVFTIKFOEFSNLMGLEQKXK 133
 QY 134 DYYIIATSDGTREGLESLOGVCLTRGMKVLRLVQG--SPRGAVPRKPVSEMPMER-DR 190
 DB 134 DYYIIATSDGTREGLESLOGVCLTRGMKVLRLVQG--SPRGAVPRKPVSEMPMER-DR 190
 QY 191 GAHSLPEKENVLPDPTSNATSRGAEPLPPSPMAVAGAGLALLLLGVAAGAGANC 250
 DB 194 GRSSTTSPVKRPPGSGSTGNSAGHGNMLLGSFVALFAGIASGCTIFVLIITLVVLL 253
 QY 251 WRRRAKPESESRHPGSGFRGSGSLGGGGGMPREAREPGLIALRGGAADPPFCPH 310
 DB 254 KYRRRRKHSPOHTTLLSLTATPRGGNN---NGSEPSDVIITFLR---TADSVFCH 306
 QY 311 YEKVSGDYGHPIYIVODGPQSPNIIYKV 340
 DB 307 YEKVSGDYGHPIYIVODGPQSPNIIYKV 336
 RESULT 15
 ADY51238
 ID ADY51238 standard; protein; 336 AA.
 XX
 XX ADY51238;
 AC
 XX 19-MAY-2005 (first entry)
 XX
 DE Mouse ephrin-B2 SEQ ID NO:7.
 XX
 XX ephrin; hematopoiesis; hyperproliferation; cytoablastic; antianemic;
 KM antiinflammatory; antipneumatic; gastroenteric; dermatological;
 KM coagulant; immunostimulant; cerebroprotective; vasotropic; antitumor.
 XX

OS Mus musculus.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 2..3
 FT /note="Optionally deleted"
 XX
 XX US2005049194-A1.
 XX
 XX 03-MAR-2005.
 XX
 XX 31-OCT-2003; 2003US-00698907.
 XX
 XX 09-NOV-2001; 2001US-0345206P.
 XX
 XX 02-JUL-2002; 2002US-0393722P.
 XX
 XX 08-NOV-2002; 2002US-00291290.
 XX
 XX 03-APR-2003; 2003US-0460488P.
 XX
 XX (FRIS/) FRISSEN J.
 XX (HOLM/) HOLMBERG J.
 XX
 XX Frissen J, Holmberg J;
 XX MPI; 2005-195317/20.
 XX
 XX Use of ephrin and its molecules for alleviating a symptom or a disorder
 XX PT with reduced levels of hematopoiesis, increased levels of cellular
 XX PT proliferation in an intestinal tract, or abnormal level of cellular
 XX PT proliferation in a tissue.
 XX
 XX Disclosure; SEQ ID NO 7; 68pp; English.
 XX
 XX The invention relates to a novel use of ephrin, ephrin inhibitors, and
 XX CC ephrin receptors for alleviating a symptom of a disorder having reduced
 XX CC levels of hematopoiesis, having increased levels of cellular
 XX CC proliferation in an intestinal tract, or having an abnormal level of
 XX CC cellular proliferation in a tissue. A composition of the invention has
 XX CC cytoablastic, antianemic, antiinflammatory, antipneumatic, gastroenteric
 XX CC -gen., dermatological, coagulant, immunostimulant, cerebroprotective,
 XX CC vasotropic, and antitumor activity. The present sequence represents
 XX CC murine ephrin-B2.
 XX
 XX Sequence 336 AA;
 SO
 Query Match 34.5%; Score 637.5; DB 9; Length 336;
 Best Local Similarity 42.1%; Pred. No. 1.8e-43;
 Matches 139; Conservative 49; Mismatches 129; Indels 13; Gaps 5;
 QY 14 GALLLLGVLGVSGLSELPYVNSANKRQAEAGGYLVLPQIGDRDLLCPRRAPRPHSS 73
 DB 17 GLMLVLCRTAISRISIVLEPIYWNSSNSKFLPGQGLVLPQIGDKDILCPKV--DSKTV 73
 QY 74 PNYEFKLYLVGAGORCEAPRPAVNLITCDRDLRFTIKFOEYSPNLMGHEFRSHN 133
 DB 74 GQYEVYKVMVDKQADRCTIKKENTPILNCARPDQVFTIKFOEFSNLMGLEQKXK 133
 QY 134 DYYIIATSDGTREGLESLOGVCLTRGMKVLRLVQG--SPRGAVPRKPVSEMPMER-DR 190
 DB 134 DYYIIATSDGTREGLESLOGVCLTRGMKVLRLVQG--SPRGAVPRKPVSEMPMER-DR 190
 QY 191 GAHSLPEKENVLPDPTSNATSRGAEPLPPSPMAVAGAGLALLLLGVAAGAGANC 250
 DB 194 GRSSTTSPVKRPPGSGSTGNSAGHGNMLLGSFVALFAGIASGCTIFVLIITLVVLL 253
 QY 251 WRRRAKPESESRHPGSGFRGSGSLGGGGGMPREAREPGLIALRGGAADPPFCPH 310
 DB 254 KYRRRRKHSPOHTTLLSLTATPRGGNN---NGSEPSDVIITFLR---TADSVFCH 306
 QY 311 YEKVSGDYGHPIYIVODGPQSPNIIYKV 340
 DB 307 YEKVSGDYGHPIYIVODGPQSPNIIYKV 336
 Search completed: December 21, 2005, 14:30:19

Thu Dec 22 11:01:45 2005

us-10-021-121-4.rag

Page 11

Job time : 114.761 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 21, 2005, 14:22:09 / Search time 20.956 Seconds
(without alignments)
1561.066 Million cell updates/sec

Title: US-10-021-121-4

Perfect score: 1850

Sequence: 1 MGPPIHSGPGVRVGLLLG.....PVYIVDGPPOSPPNIYKY 340

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	637.5	34.5	336	2	I49766	hepatoma transmem
2	632	34.2	346	2	S46993	elk ligand - human
3	629.5	34.0	333	2	I84743	hepatoma transmem
4	613.5	33.2	345	2	I48780	Strat/Sp1g2 protei
5	608.5	32.9	345	2	I58406	LERR-2 - rat
6	214.5	11.6	237	2	T19914	hypothetical prote
7	179	9.7	238	2	I38849	LERR-3 - human
8	176	9.5	209	2	A54984	ELF-1 protein prec
9	175.5	9.5	213	2	JE0322	ephurin-A2 - human
10	170.5	9.2	228	2	A57084	repulsive axon gult
11	169.5	9.2	201	2	I38850	LERR-4 - human
12	167.5	9.1	228	2	I58170	LERR-7 precursor -
13	166	9.0	205	2	A36377	Bcl protein precu
14	159	8.6	680	2	S31216	collagen alpha 1(X
15	154.5	8.4	1049	1	CG8075	collagen alpha 1(I
16	153.5	8.3	1670	1	CGHJ3B	collagen alpha 3(I
17	151.5	8.2	301	2	B31219	collagen 2 - Caen
18	149	8.1	325	2	T32248	hypothetical prote
19	149	8.1	569	2	S42886	collagen - silkwo
20	148.5	8.0	316	2	T20497	hypothetical prote
21	148	8.0	921	2	S42617	collagen alpha 1(I
22	146.5	7.9	1315	2	A56101	collagen alpha 1(X
23	146.5	7.9	1492	2	A40333	collagen alpha 1(X
24	146.5	7.9	1774	2	B56101	collagen alpha 1(X
25	146	7.9	675	2	S20819	collagen alpha 3(I
26	145.5	7.9	305	2	T20906	hypothetical prote
27	145	7.8	974	2	S13301	collagen alpha 1(X
28	145	7.8	931	2	S13580	collagen alpha 1(I
29	144.5	7.8	438	2	S53787	collagen alpha cha

30	144	7.8	1027	2	S28774	collagen alpha cha
31	143	7.7	1747	2	A54121	collagen alpha-4 c
32	142.5	7.7	743	1	S23779	collagen alpha 1(V
33	142.5	7.7	1496	1	CGHJ2V	collagen alpha 2(V
34	142	7.7	744	2	S15435	collagen alpha 1(V
35	142	7.7	1029	1	S21369	collagen alpha 2(V
36	142	7.7	1763	2	S16366	collagen alpha 1(I
37	141.5	7.6	1466	1	CGHJ7L	collagen alpha 1(I
38	141	7.6	319	2	T32250	hypothetical prote
39	141	7.6	744	1	A34246	collagen alpha 1(V
40	141	7.6	744	1	S23298	collagen alpha 1(V
41	140.5	7.6	305	2	T30165	hypothetical prote
42	140	7.6	304	2	T22482	hypothetical prote
43	140	7.6	680	1	CGHJ1D	collagen alpha 1(X
44	139.5	7.5	210	2	B44984	collagen - nematod
45	139	7.5	940	2	JE0291	FB19 protein - hum

ALIGNMENTS

RESULT 1

I49766
hepatoma transmembrane kinase ligand - mouse
C/Species: Mus musculus (house mouse)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C/Accession: I49766
R/Bennett, B.D.; Zeigler, F.C.; Gu, O.; Fendly, B.; Goddard, A.D.; Gillett, N.; Matthews, Proc. Natl. Acad. Sci. U.S.A. 92, 1866-1870, 1995
A/Title: Molecular cloning of a ligand for the Eph-related receptor protein-tyrosine kinase
A/Reference number: I49766; MUID:95199254; PMID:7534404
A/Accession: I49766
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-336 <RES>
A/Cross-references: UNIPROT:P52800; UNIPARC:UPI000020B55; GB:I38847; NID:g769677; PIDD:I
A/Genes: HTK

Query Match 34.5%; Score 637.5; DB 2; Length 336;

Best Local Similarity 42.1%; Pred. No. 1.3e-37;

Matches 139; Conservative 49; Mismatches 129; Indels 13; Gaps 5;

QY	14	GALLLVGLVGSGLSPVYVNSANKRFOAGGYVLPQIGPDLICPRAPPSS 73	
DB	17	GLMLVLCRTAIRSIVLEPIYMNSSKFLPGGLVLYFOIGDKLIIICKV--DSKY 73	
QY	74	PNYEFYKLVVGAQGRCEAPPAVNLITCDRPDLLEFTIKFOEYSPNLWGHEFRSH 133	
DB	74	GQVEYKVMVNDQADRCIKKENTPLNLCARPDQVFTIKFOEYSPNLWGHEFRSH 133	
QY	134	DYVITATSDGTREGLSLOGGVCLITGMKYLVRVG--SPRGCAVRRKPYSEPMER-DR 190	
DB	134	DYVITATSDGTREGLSLOGGVCLITGMKYLVRVG--SPRGCAVRRKPYSEPMER-DR 190	
QY	191	GAHSLPEPKENLPGDPTSNATSRGAEGPLPPPSMAVGAAGALLLLVGAAGAGMC 250	
DB	194	GRSSTSPVKKPSPGSSDTGNSAGHGNNLGSSEVLFAGIASGCIIFVITLVVLL 253	
QY	251	WRRRAKPSRSRRPFGSGSLGIGGGGGMGPAREPGEIGIALRGGAADPPFCPH 310	
DB	254	KYRRRRKHSPOHTTLLSLTSLATLTPKGGNN-----NGSEPSDVIPLR---TADSVFCPH 306	
QY	311	YKVSQDYGHPVYIVDGPPOSPPNIYKY 340	
DB	307	YKVSQDYGHPVYIVDGPPOSPPNIYKY 336	

RESULT 2

S46993
elk ligand - human
C/Species: Homo sapiens (man)
C/Date: 15-Jul-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004


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Db      189 VKT-----ATQAPRGSGQSDSGKHETVNOEKSGAGGSGSDSFNSK 236
Qy      237 LLLLVGAGAGA-----NCWRRRAKPSSESRHPGSGFGSGSLGL-----CG 279
Db      237 VALFAVAGACVFLIIITFLVLLKTKRKRKHQO-----RAAALSISLASP 287
Qy      280 GGGMGPREAPGELGIALRGGAADPPFCPHYEKVSVDYGHPIYIVQDPPGSPNNIYK 339
Db      288 KGGSGTAGTEPSPDIIIPLR---TTENNYCPHYEKVSGDYGHPIYIYQEMPPGSPANNIYK 344
Qy      340 V 340
Db      345 V 345

RESULT 5
158406
LEKR-2 - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C:Accession: I58406
R:Piecher, F.A.; Carpenter, M.; Shilling, H.; Baum, P.; Ziegler, S.; Hollin
Oncogene 9, 3243-3248, 1994
A:Title: LEKR-2, a ligand for the receptor tyrosine kinase Elk, is evolutionarily conserved
A:Reference number: I58406; MUID:95022634; PMID:7936648
A:Accession: I58406
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-345 <RES>
A:Cross-references: UNIPROT:P52796; UNIPARC:UPI0000129C98; EMBL:U07560; NID:9563118; PID
A:Gene: Bp1g2

Query Match      32.9%; Score 608.5; DB 2; Length 345;
Best Local Similarity 38.0%; Pred. No. 1.4e-35;
Matches 137; Conservative 52; Mismatches 107; Indels 65; Gaps 10;

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Qy      15 ALLILGLVLSGL--SLRPVYWNANKRPOAEGVLYLPQIGDRLLICPRARPPGHS 72
Db      15 ANAVLTLCLATPLATLAPLALPVSWSLNPXFLSGKGLVTPKIGDKLDIICPRAEAGRP-- 72
Qy      73 SPNVEFYKLYLVGAQGRCEAPAPNLLITCDRPLDLRTIKFOEYSPNLMGHEFRSH 132
Db      73 ---YEVYKLYLVREDAACSTVLDPNVLTCKPQOEIRFTIKFOEFSPNMGLEFKY 129
Qy      133 HDYIYIATSDGTREGLESLOGGVCLTRGMKVLIRVQSGSPRGAVPKPVSEMERDRA 192
Db      130 HDYIYITSTNGSLGLEENREGVCRTRTMKIWMKVQODP-NAVTPQQLTTSRPSKESDNT 188
Qy      193 AISLEGRKNLPODPTSNATSRGAEPR-----LPPSPMAYAVAGAG-----LA 236
Db      189 VKT-----ATQAPRGSGQSDSGKHETVNOEKSGAGGSGSDSFNSK 236
Qy      237 LLLLVGAGAGA-----NCWRRRAKPSSESRHPGSGFGSGSLGL-----CG 279
Db      237 VALFAVAGACVFLIIITFLVLLKTKRKRKHQO-----RAAALSISLASP 287
Qy      280 GGGMGPREAPGELGIALRGGAADPPFCPHYEKVSVDYGHPIYIVQDPPGSPNNIYK 339
Db      288 KGGSGTAGTEPSPDIIIPLR---TTENNYCPHYEKVSGDYGHPIYIYQEMPPGSPANNIYK 344
Qy      340 V 340
Db      345 V 345

RESULT 6
T19914
Hypothetical protein C43F9.8 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T19914

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R:Northmore, B.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z19195
A:Accession: T19914
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-237 <WIL>
A:Cross-references: UNIPROT:Q9U3M2; UNIPARC:UPI0000078016; EMBL:Z622262; PID:CA854195.1;
A:Experimental source: clone C43F9
C:Genetics:
A:Gene: CESP:C43F9.8
A:Map position: 4 96/3; 214/1
A:Introns: 32/2; 96/3; 214/1

Query Match      11.6%; Score 214.5; DB 2; Length 237;
Best Local Similarity 25.7%; Pred. No. 4.1e-08;
Matches 53; Conservative 41; Mismatches 83; Indels 29; Gaps 6;

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Qy      11 VRVGLALLGLVGLVS-GISLEPVYWNANKRPOAEG-GVLYLPQIGDRLLICPRARPP 68
Db      1 MQIATPILSLPPIGMAKIPDIMWISSNPFDVSNTHVTSVHIGDRVSIKCPKSDRT 60
Qy      69 GRHSSPNVEFYKLYLVGAQGRCEAPAPNLLITCDRPLDLRTIKFOEYSPNLMGHE 128
Db      61 G-----KYEYSYIYVWSDEYDHCFI-SKRLVGAACDNOTINAGINIVFRSFTTPGFE 114
Qy      129 FRSHHDYIIA-----TSDGTREGLESLOGGVCLTRGMKVLIRVQ 169
Db      115 FQPGKNYFLIISSEVDALITETANOIFPGTSDGLTLEGIDRKDDGLCTAKMKIKFEVQ 174
Qy      170 SPRGAVPRKPVSEMERDRAAHS 195
Db      175 DRRTIENPK--FAARTLKKDRDAHS 198

RESULT 7
138849
LEKR-3 - human
C:Species: Homo sapiens (man)
C>Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C:Accession: I38849
R:Kozlovsky, C.U.; Marakovskiy, E.; McGrew, J.T.; Vandenbos, T.; Teepe, M.; Lyman, S.D.; &
Oncogene 10, 299-306, 1995
A:Title: Ligands for the receptor tyrosine kinases hek and elk: isolation of cDNAs encoding
A:Reference number: I38849; MUID:95140419; PMID:7838529
A:Accession: I38849
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-238 <RES>
A:Cross-references: UNIPROT:P52797; UNIPARC:UPI0000129C9F; EMBL:U14187; NID:9642832; PID
A:Gene: GDB:EPLG3
A:Cross-references: GDB:438336; OMIM:601381
A:Map position: 1q21-1q22
C:Superfamily: axon guidance signal protein

Query Match      9.7%; Score 179; DB 2; Length 238;
Best Local Similarity 28.4%; Pred. No. 1.3e-05;
Matches 65; Conservative 24; Mismatches 80; Indels 60; Gaps 12;

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Qy      7 GPGGVAVGALLGLVGLVSGLSEPVYWNANKRPOAEGVLYLPQIGDRLLICPRARPP 64
Db      24 GPG-----GALG-----NRRAVYWNSSNGHLRR-GTVQVNVVDYDIDYCPHN 67
Qy      65 APPGPHSP-----NYEFKLYLVGAQGRCEAPAPNLLITCDRPLD--DLRFTIKF 117
Db      68 SSGVGAGAGPAGGAGAGVLYLVVGRNGYRTCNAGQFK-RWECNRPHAPHSPIKSEKF 126
Qy      118 QEYSPNLMGHEFRSHHDYIITSDGTREGLESLOGGVCLTRGMKVLIRVQSPRGAAP 177
Db      127 QRYSAFSLGVEFHAGIEYIISTPTNHL-----WKCLR--MKVFPCCASTSHSG--- 174
Qy      176 RKPVSSEMP-----MERDRGAHSLB-----PKENILP 204

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C:Superfamily: axon guidance signal protein

Query Match 9.2%; Score 169.5; DB 2; Length 201;
 Best Local Similarity 29.9%; Pred. No. 5e-05;
 Matches 66; Conservative 18; Mismatches 82; Indels 55; Gaps 10;

QY 24 LVVGLSL-EPVYVNSANKRFOAEGGYLYPQIGDRLDLCPRARPFGPHSSPNVEFYKLY 82
 DB 20 LRGSSLRHYVYVNSNPNRL-LRGDAVVELGLNDYDIVEPHNGEGPPGPG--ETFPALY 76
 QY 83 LVGGAQGRRCAP-PAPNLLITCDRDPDLRFITKFOEYSPNLMGHEFRSHDYITIAN 141
 DB 77 MYDWPVEYSCQAAGPAPYAKKWCSLPFGHVQFSEKIQRFPSLGFEPFLGCTYYIISVP 136
 QY 142 DGRREGLESQGVCLTRGMKVLRLVQSPRGGAIVRRKPPVSEMPMERDRGAHSLRPGKE 201
 DB 137 --TPE-----SSQQL-----RLQYVCCCKERSAHAV----- 164

QY 202 NLPGDPTSNAT--RGAEGLPPSPMPAVAGAGLALLL 240
 DB 165 ---GSFGESGTSGMRCGDTSP-----LCILL 189

RESULT 12

158170
 LERK-7 precursor - human
 N:Alternate names: AL-1
 C:Species: Homo sapiens (man)
 C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
 C:Accession: 158170; GI1812
 R:Wimlow, J.W.; Moran, P.; Valverde, J.; Shih, A.; Yuan, J.Q.; Wong, S.C.; Tsai, S.P.; Neuron 14, 973-981 1995
 A>Title: Cloning of AL-1, a ligand for an Eph-related tyrosine kinase receptor involved
 A:Reference number: 158170; MID:95267434; PMID:7748564
 A:Accession: 158170
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-228 <RES>
 A:Cross-references: UNIPROT:P52803; UNIPARC:UPI0000129C93; GB:S77167; NID:g914184; PID:g
 R:Kozlovsky, C.J.; Vandenhoe, T.; Park, U.S.; Cerretti, D.P.; Carpenter, M.K.
 submitted to the EMBL Data Library, May 1995
 A:Reference number: G08477
 A:Accession: G01812
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-228 <KOZ>
 A:Cross-references: UNIPARC:UPI0000129C93; EMBL:U26403; NID:g1019430; PIDN:AA60377.1; F
 A:Gene: GDB:EP167; APL; LERK7
 A:Cross-references: GDB:568757; OMIM:601535
 A:Map position: 13q33-13q33
 C:Superfamily: axon guidance signal protein

Query Match 9.1%; Score 167.5; DB 2; Length 228;
 Best Local Similarity 28.8%; Pred. No. 7.9e-05;
 Matches 65; Conservative 29; Mismatches 81; Indels 51; Gaps 11;

QY 33 VYVNSANKRFOAEGGYLYPQIGDRLDLCPRARPFGPHSSPNVEFYKLYLVG----- 85
 DB 34 VYVNSNPNRFO-RGDYHIDVICINDYLDVFCPHYEDSVPEDKT--ERYLYVMVDFGYSAC 90
 QY 86 -----CAQGRRCAPAPNLLITCDRDPDLRFITKFOEYSPNLMGHEFRSHDYITIAN 140
 DB 91 DHTSKFGPKMECRPHSPN-----GPLKSEKFOLETPSLGPEPRPGREYFYS 141
 QY 141 S---DGRREGLESQGVCLTRGMKVLRLVQSPRGGAIVRRKPPVSEMPMERDRGAHSLR 197
 DB 142 ALPDNRRS-----CLK--LKFVVR-----PTNSCKTTIGVHRVDPVNDKVENSLR 186
 QY 198 PCKENLPGDPTSNATSGAEGPLPPSPMPAVAGAGLALLLIGVA 243
 DB 187 PADDTV---HSAEPERG--ENAAQTPIRISRL-----LAILFLLA 223

RESULT 13

A36377
 B61 protein precursor - human
 C:Species: Homo sapiens (man)
 C>Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 09-Jul-2004
 C:Accession: A36377
 R:Holzman, L.B.; Marks, R.M.; Dixit, V.M.
 Mol. Cell. Biol. 10, 5830-5838, 1990
 A>Title: A novel immediate-early response gene of endothelium is induced by cytokines and
 A:Reference number: A36377; MID:91042512; PMID:2233719
 A:Accession: A36377
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-205 <HOL>
 A:Cross-references: UNIPROT:P20827; UNIPARC:UPI0000129C89; GB:M57730; GB:M37476; NID:g175
 C:Superfamily: axon guidance signal protein

Query Match 9.0%; Score 166; DB 2; Length 205;
 Best Local Similarity 27.5%; Pred. No. 8.9e-05;
 Matches 46; Conservative 31; Mismatches 74; Indels 16; Gaps 5;

QY 18 LVGLVGLVSL-EPVYVNSANKRFOAEGGYLYPQIGDRLDLCPRARPFGPHSSPN-- 75
 DB 8 LVGLCCSLAAADRHTVFNNSNPKFRNE-DYTIHVQLNDYVDITCPHYE---DHSVADAA 63
 QY 76 YEFYKLYVGAQGRRCAPAPNLLITCDRDPDL--DARFTTKFOEYSPNLMGHEFRSH 132
 DB 64 MEQYILYLVHEHEYOQCPQSKDYVWQCNRRSARKGPEKLEKFRFTPLTGKEFKG 123
 QY 133 HDYIYIATSDGREGLESQGVCLTRGMKVLRLVQSPRGGAIVRRK 179
 DB 124 HSYIYSKRIHQHQR-----CLRLKTYVSGKITHSQAVNVPQS 163

RESULT 14

S31216
 collagen alpha 1(X) chain precursor - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
 C:Accession: S31216; S28807; S2215; S30127; 148299; S26397; S31830
 R:Kong, R.Y.C.; Kwan, K.M.; Lau, E.T.; Thomas, J.T.; Boot-Handford, R.P.; Grant, M.E.; Cl
 Eur. J. Biochem. 213, 99-111, 1993
 A>Title: Intron-exon structure, alternative use of promoter and expression of the mouse c
 A:Reference number: S31216; MID:93238750; PMID:8477738
 A:Accession: S31216
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-680 <KON>
 A:Cross-references: UNIPROT:O05306; UNIPARC:UPI000016CBAA; EMBL:Z21610; NID:g49793; PIDN
 R:Elima, K.; Berola, I.; Rosati, R.; Metsaeranta, M.; Garofalo, S.; Peracalo, M.; de Cro
 Biochem. J. 289, 247-253, 1993
 A>Title: The mouse collagen X gene: complete nucleotide sequence, exon structure and exp
 A:Reference number: S28807; MID:93143676; PMID:8424763
 A:Accession: S28807
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-285; A', 287-680 <E1>
 A:Cross-references: UNIPARC:UPI0000026913; EMBL:X67348; NID:g50480; PIDN:CAA47763.1; PID
 R:Elima, K.; Metsaeranta, M.; Kallilo, J.; Peracalo, M.; Berola, I.; Garofalo, S.; de Cro
 Biochem. Biophys. Acta 1130, 78-80, 1992
 A>Title: Specific hybridization probes for mouse alpha-2(IX) and alpha-1(X) collagen mRN
 A:Reference number: S22215; MID:92182017; PMID:1543751
 A:Accession: S22215
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 385-450; 'K', 452-627 <ELA>
 A:Cross-references: UNIPARC:UPI000016CBAB; EMBL:X63013; NID:g49795; PIDN:CAA44741.1; PID
 R:Adle, S.S.; Olsen, B.R.
 Matrix 13, 165-179, 1993
 A>Title: Characterization of the mouse type X collagen gene.
 A:Reference number: S30127; MID:93261348; PMID:8492743
 A:Accession: S30127
 A:Status: preliminary
 A:Molecule type: mRNA

A:Residues: 1-12, 'F', 14-26, 'S', 28-247, 'L', 249-285, 'A', 287-305, 'F', 307-416, 'S', 418-499, 'L'
A:Cross-references: UNIPARC:UPI00001773B5
R:Appte, S.S.; Seidlin, M.F.; Hayaishi, M.; Olsen, B.R.
Eur. J. Biochem. 206, 217-224, 1992
A:Title: Cloning of the human and mouse type X collagen genes and mapping of the mouse
A:Reference number: 148299; PMID:92267014; PMID:1587271
A:Accession: 148299
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 52-247, 'L', 249-285, 'A', 287-305, 'F', 307-416, 'S', 418-499, 'L', 501-566, 'C', 568, 'F'
A:Cross-references: UNIPARC:UPI000016CCAC; EMBL:X65121; NID:G50482; PIDN:CA46237.1; PID
R:Summers, T.A.; Irwin, M.H.; Mayne, R.; Balian, G.
J. Biol. Chem. 263, 581-587, 1988
A:Title: Monoclonal antibodies to type X collagen. Biosynthetic studies using an antibody
A:Reference number: S26397; PMID:88087150; PMID:2826450
A:Accession: S26397
A:Molecule type: protein
A:Residues: 'SDGYFQ', 24-26, 'KQ', <SUM>
A:Cross-references: UNIPARC:UPI00001773B6
C:Genetics:
A:Gene: Col10a-1
A:Map position: 10
A:Introns: 51/3
C:Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homology
C:Keywords: coiled coil; extracellular matrix; glycoprotein; homotrimer
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-680/Product: collagen alpha 1(X) chain #status predicted <MAT>
F:553-679/Domain: complement C1q carboxyl-terminal homology <C1Q>

Query Match 8.4%; Score 159; DB 2; Length 680;
Best Local Similarity 25.5%; Pred. No. 0.001;
Matches 97; Conservative 30; Mismatches 108; Indels 146; Gaps 24;

QY 1 MGPHSGPGGV-RVGAALLLGLVGLSGLSLEPVYNNANKRQAEQGYLYPQIGDRLD 59
DB 211 IGP- -GPSCVGRGNGPFGPGI- - - - -KDRGPGEMG- - - - - 244
QY 60 LLCPRARPGPHSSPYVEFYKLYLVGAQGRCEAPAPNLLTCRDLNFTIKFOE 119
DB 245 - - - - -PGSPGPGQPF- - - - -GKQGR-EGIGKPGALISPGQPGI- - - - - 277
QY 120 YENMLGHERSHNDYIIITSTGT- - - - -REGLESLOGVCLTRGNKVLRLVQSPRGA 175
DB 278 - - - - -PGEKHGPGSPG- - - - -IAGPPGAPGFGKQSPGLRG- - - - -ORG- - - - -PAG- - - - - 314
QY 176 VPKPYSEMPMERDRGAHSLERQKENTLPGDPTSNATSRGAEGLPPSPMAVAGAAG 235
DB 315 LEPAPG- - - - -KGERPAG- - - - -HGEFGLPESP- - - - -GNMGPGPKGIPGNHGIPGAKGEI 364
QY 236 ALLLLGVAGAGACWRRRRAR- - - - -SESRHPG- - - - -PGSFRGSGLGLGGGG 282
DB 365 G- - - - -LVGPAPGPGA- - - - -RGARPGPLDGKTGYPGEPGLNGPKNGRLPGQGDPDGVGCTPG 419
QY 283 M- - - - - - - - - - -GPREAPGELGLLRGGGAADPPFCHEYVNSDYPHY 323
DB 420 LRGPVPGVAKGVPGHNGEAGPR-GEFGIIPGTR- - - - -GTPPGPVGPFPGSKCDPNNP- - - - - 472
QY 324 IVQDGP- - - - - - - - - - -PGSP 334
DB 473 -GAPGAPGATTKLNGPTGPP 492

RESULT 15

CG8075
collagen alpha 1(III) chain - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 04-Dec-1986 #sequence revision 04-Dec-1986 #text change 09-Jul-2004
C:Accession: A02862; A38001; A38002; A38003; A38004; A38005; S71946
R:Fietzek, P.P.; Allmann, H.; Rauterberg, J.; Henkel, W.; Wachter, E.; Kuehn, K.
Hoppe-Seyler's Z. Physiol. Chem. 360, 809-820, 1979
A:Title: The covalent structure of calf skin type III collagen. I. The amino acid sequen
A:Reference number: A02862; PMID:80026026; PMID:488906
A:Accession: A02862

A:Molecule type: protein
A:Residues: 1-242 <FIR>
A:Cross-references: UNIPROT:P04258; UNIPARC:UPI0000173B8A
R:Dewes, H.; Fietzek, P.P.; Kuehn, K.
Hoppe-Seyler's Z. Physiol. Chem. 360, 821-832, 1979
A:Title: The covalent structure of calf skin type III collagen. II. The amino acid sequen
A:Reference number: A38001; PMID:80026027; PMID:488907
A:Accession: A38001
A:Molecule type: protein
A:Residues: 243-422 <DEW1>
A:Cross-references: UNIPARC:UPI0000173B8B
R:Benz, H.; Fietzek, P.P.; Kuehn, K.
Hoppe-Seyler's Z. Physiol. Chem. 360, 833-840, 1979
A:Title: The covalent structure of calf skin type III collagen. III. The amino acid sequen
A:Reference number: A38002; PMID:80026028; PMID:488908
A:Accession: A38002
A:Molecule type: protein
A:Residues: 423-571 <BEN>
A:Cross-references: UNIPARC:UPI0000173B8C
R:Lang, H.; Glanville, R.W.; Fietzek, P.P.; Kuehn, K.
Hoppe-Seyler's Z. Physiol. Chem. 360, 841-850, 1979
A:Title: The covalent structure of calf skin type III collagen. IV. The amino acid sequen
A:Reference number: A38003; PMID:80026029; PMID:488909
A:Accession: A38003
A:Molecule type: protein
A:Residues: 572-808 <LAN>
A:Cross-references: UNIPARC:UPI0000173B8D
R:Dewes, H.; Fietzek, P.P.; Kuehn, K.
Hoppe-Seyler's Z. Physiol. Chem. 360, 851-860, 1979
A:Title: The covalent structure of calf skin type III collagen. V. The amino acid sequen
A:Reference number: A38004; PMID:80026030; PMID:488910
A:Accession: A38004
A:Molecule type: protein
A:Residues: 809-947 <DEW2>
A:Cross-references: UNIPARC:UPI0000173B8E
R:Allmann, H.; Fietzek, P.P.; Glanville, R.W.; Kuehn, K.
Hoppe-Seyler's Z. Physiol. Chem. 360, 861-868, 1979
A:Title: The covalent structure of calf skin type III collagen. VI. The amino acid sequen
A:Reference number: A38005; PMID:80026031; PMID:488911
A:Accession: A38005
A:Molecule type: protein
A:Residues: 948-1049 <ALL>
A:Cross-references: UNIPARC:UPI0000173B8F
A:Experimental source: skin
R:Henkel, W.
Biochem. J. 318, 497-503, 1996
A:Title: Cross-link analysis of the C-telopeptide domain from type III collagen.
A:Reference number: S71946; PMID:96404897; PMID:8809038
A:Accession: S71946

A:Molecule type: protein
A:Residues: 87-106;1017-1029;1037-1049 <HEN>
A:Cross-references: UNIPARC:UPI0000173B90; UNIPARC:UPI0000173B91; UNIPARC:UPI0000173B92
C:Comment: Prolines at the third position of the tripeptide repeating unit (G-X-Y) are by
C:Superfamily: collagen alpha 1(III) chain; fibrillar collagen carboxyl-terminal homology;
C:Keywords: coiled coil; extracellular matrix; glycoprotein; hydroxylysine; hydroxyprolin
F:1-1049/Product: collagen alpha 1(III) chain #status experimental <CAB>
F:1-14/Region: amino-terminal nonhelical telopeptide
F:15-1040/Region: helical
F:587-589/Region: cell attachment (R-G-D) motif
F:752-754/Region: cell attachment (R-G-D) motif
F:875-877/Region: cell attachment (R-G-D) motif
F:878-880/Region: cell attachment (R-G-D) motif
F:935-937/Region: cell attachment (R-G-D) motif
F:1041-1049/Region: carboxyl-terminal nonhelical telopeptide
F:95;107,119,938,950/Modified site: 5-hydroxylysine (lys) #status experimental
F:107,950/Modified site: allysine (lys) #status predicted
F:107/Binding site: carboxylate (lys) (covalent) #status experimental
F:1040,1041/Disulfide bonds: interchain #status predicted

Query Match 8.4%; Score 154.5; DB 1; Length 1049;
Best Local Similarity 26.5%; Pred. No. 0.0034; Indels 83; Gaps 8;
Matches 60; Conservative 9; Mismatches 74;

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QY      171 PRGGAVPRKRVSEVEMPERRG-----ASHLEEGKEN 202
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Db      688 PAGSGCPACPPGPGQGVKERGSFGCGPAAAGPCGGRCPGCPGSGNSGNPGRPSSGAHGKD 747
          :::|||
QY      203 LPGDSTSNAT-----SRGAEEPLPPSPMAVAGAAGLALLLLLVAGA 245
          |||||
Db      748 PGPGFSGSNGAPGSPGISCPKDGSDGPPGERGAPGPDPGPAPGLIAG----LTGARGL 802
          |||||
QY      246 GGAMCWRRRRAKP-----SESRLHPG-----GSFRKGSLIGLGCGGGMGPREABPGE 292
          |||||
Db      803 AGPPGMPPGARPGSPFOGIKGENGKPEPSGONGERGHPPGQGLGTAGTAGEPGRDGNPGS 862
          |||||
QY      293 LGIALRGG-----GADNPFCCHYEKVSGDYGHPIVTVDNQP 330
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Db      863 DGLPGRDGA PGA KIDRGENGSPAP-----GAPGHP-----GPP 896
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Search completed: December 21, 2005, 14:36:32
Job time : 21.956 sec8

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: December 21, 2005, 14:21:53 ; Search time 131.723 Seconds
(without alignments)
1821.088 Million cell updates/sec

Title: US-10-021-121-4

Perfect score: 1850
Sequence: 1 MGPSPHSGPGVGVALLIG.....PVYVQDGPSPSPNYYKV 340

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : UniProt_05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1850	100.0	340	1 EFN83_HUMAN	Q15768 homo sapien
2	1780	96.2	340	2 EFN83_MOUSE	O35393 mus musculu
3	1780	96.2	340	2 O5F221_MOUSE	O5F221 mus musculu
4	923	49.9	331	2 O90231_BRARE	O90231 brachydanio
5	923	49.9	342	2 O50203_BRARE	O50203 brachydanio
6	919	49.7	327	2 O9PT69_XENLA	O9PT69 xenopus lae
7	637.5	34.5	336	1 EFN82_MOUSE	P52800 mus musculu
8	637.5	34.5	336	2 O4FJM3_MOUSE	O4FJM3 mus musculu
9	632	34.2	346	1 EFN81_HUMAN	P98172 homo sapien
10	629.5	34.0	333	1 EFN82_HUMAN	P52799 homo sapien
11	629.5	34.0	333	2 O5JVS6_HUMAN	O5JVS6 homo sapien
12	629.5	34.0	333	2 O9PUJ4_CHICK	O9PUJ4 gallus gall
13	628	33.9	334	1 EFN81_CHICK	O73612 gallus gall
14	626.5	33.9	332	1 EFN82_BRARE	O73874 brachydanio
15	616	33.3	341	2 O90233_BRARE	O90233 brachydanio
16	613.5	33.3	345	2 O6P7B6_RAT	O6P7B6 rattus norv
17	613.5	33.2	345	1 EFN81_MOUSE	P52795 mus musculu
18	613.5	33.2	345	2 O54419_MOUSE	O54419 mus musculu
19	608.5	32.9	345	1 EFN81_RAT	P52796 rattus norv
20	605.5	32.7	329	2 O6PFS3_XENLA	O6PFS3 xenopus lae
21	605.5	32.7	334	2 O90232_BRARE	O90232 brachydanio
22	600	32.4	327	1 EFN81_XENLA	O13097 xenopus lae
23	568.5	30.7	324	2 O4SHZ6_TETNG	O4SHZ6 tetraodon n
24	452	24.4	304	2 O4T7D5_TETNG	O4T7D5 tetraodon n
25	401	21.7	386	2 O4RK83_CIOIN	O4RK83 ciona intes
26	349.5	18.9	359	2 O4H318_CIOIN	O4H318 ciona intes
27	341.5	18.5	217	2 O5JVS7_HUMAN	O5JVS7 homo sapien
28	340	18.4	205	2 O9R6H9_XENLA	O9R6H9 xenopus lae
29	251.5	13.6	97	2 O4RZ21_TETNG	O4RZ21 tetraodon n
30	239.5	12.9	212	2 O61WH3_CABER	O61WH3 caenorhabd
31	234	12.6	218	2 O9U3M2_CABER	O9U3M2 caenorhabd

32	214	11.6	182	2 O4RT95_TETNG	O4RT95 tetraodon n
33	198.5	10.7	279	2 O9U474_CABER	O9U474 caenorhabd
34	198	10.7	278	2 O61HF9_CABER	O61HF9 caenorhabd
35	185	10.0	195	1 EFN82_BRARE	P79727 brachydanio
36	184.5	10.0	428	2 O5TXC6_ANOGA	O5TXC6 anopheles g
37	182	9.8	260	2 O6V049_MANSE	O6V049 manucea sex
38	182	9.8	652	2 O9V4E1_DROME	O9V4E1 drosophila
39	179	9.7	238	1 EFN83_HUMAN	P52797 homo sapien
40	178.5	9.6	202	2 O98RT2_CHICK	O98RT2 gallus gall
41	176	9.5	209	1 EFN82_MOUSE	P52801 mus musculu
42	175.5	9.5	213	1 EFN82_HUMAN	O43921 homo sapien
43	172.5	9.3	217	2 O5M7P3_XENTR	O5M7P3 xenopus tro
44	172	9.3	200	1 EFN82_CHICK	P52802 gallus gall
45	170.5	9.2	228	1 EFN85_CHICK	P52804 gallus gall

ALIGNMENTS

RESULT 1
EFN83_HUMAN STANDARD; PRT; 340 AA.
AC Q15768; O00680; Q8TBH7; Q92875;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Bphrin-3 precursor (EPH-related receptor tyrosine kinase ligand 8)
DE (LEK8-8) (EPH-related receptor transmembrane ligand ELK-L8).
GN Name=EFN83; Synonyms=EPD8, LEK8;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Cerretti D.P.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=9771551; PubMed=9126477; DOI=10.1006/geno.1997.4615;
RA Tang X.X., Pleasure D.E., Ikegaki N.;
RT "CDNA cloning, chromosomal localization, and expression pattern of
RT EPH8, a new member of the EPH gene family encoding ligands of EPH-
RL related protein-tyrosine kinase receptors.";
RL Genomics 41:17-24(1997).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain cortex;
RX MEDLINE=96404527; PubMed=8808709;
RA Gale N.W., Flemken A., Compton D.C., Jenkins N.A., Copeland N.G.,
RA Gilbert D.J., Davis S., Wilkinson D.G., Yancopoulos G.D.;
RT "Elk-13, a novel transmembrane ligand for the Eph family of receptor
RT tyrosine kinases, expressed in embryonic floor plate, roof plate and
RT hindbrain segments.";
RL Oncogene 13:1343-1352(1996).
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Alteschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stappleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Mollath S.J.,
RA Raha S.S., Iqbal N.A., Peters G.J., Abrahamson R.D., Mollath S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.U., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.W., Gay L.J., Huijck S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
FAhey J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield V.S.N., Krzywincki M.I., Skalska U., Smalins D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RP PROTEIN SEQUENCE OF 28-42.
 RX PubMed=15340161; DOI=10.1110/ps.04682504;
 RA Zhang Z., Henzel W.J.,
 RT "Signal peptide prediction based on analysis of experimentally
 RT verified cleavage sites.";
 RL Protein Sci. 13:2819-2824(2004).
 RN [6]
 RP INTERACTIONS WITH GRIP1 AND GRIP2.
 RC TISSUE=Fetal brain.
 RX MEDLINE=99211388; PubMed=10197531; DOI=10.1016/S0896-6273(00)80706-0;
 RA Brueckner K., Pablo Labrador J., Scheffele P., Herb A., Seeburg P.H.,
 RA Klein R.,
 RT "EphrinB ligands recruit GRIP family PDZ adaptor proteins into raft
 RT membrane microdomains.";
 RL Neuron 22:511-524(1999).
 CC -1- FUNCTION: May play a pivotal role in forebrain function. Binds to,
 CC and induce the collapse of, commissural axons/growth cones in
 CC vitro. May play a role in constraining the orientation of
 CC longitudinally projecting axons (By similarity).
 CC -1- SUBUNIT: Interacts with GRIP1 and GRIP2.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: Highly expressed in brain; expressed in
 CC embryonic floor plate, roof plate and hindbrain segments.
 CC -1- SIMILARITY: Belongs to the ephrin family.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL; U57001; AAB05170.1; -; mRNA.
 DR EMBL; U6406; AAC51203.1; -; mRNA.
 DR EMBL; U62775; AAC50707.1; -; mRNA.
 DR EMBL; BC024399; AAH24399.1; -; mRNA.
 DR EMBL; BC042944; AAH42944.1; -; mRNA.
 DR HSSP; P52800; 1IKO.
 DR Ensembl; ENSG00000108947; Homo sapiens.
 DR HGNC; HGNC:3228; EFNB3.
 DR MIM; 602297; -.
 DR GO; GO:0005887; C:Integral to plasma membrane; TAS.
 DR GO; GO:0005005; F:Transmembrane-ephrin receptor activity; TAS.
 DR GO; GO:0007267; P:cell-cell signaling; TAS.
 DR GO; GO:0007399; P:neurogenesis; TAS.
 DR InterPro; IPR001799; Ephrin.
 DR Pfam; PF00812; Ephrin.1.
 DR PRINTS; PR01347; EPHRIN.
 DR ProDom; PD002533; Ephrin.1.
 DR PROSITE; PS01239; EPHRIN.1.
 KW Developmental protein; Differentiation; Direct protein sequencing;
 KW Glycoprotein; Neurogenesis; Polymorphism; Signal; Transmembrane.
 FT SIGNAL 1 27
 FT CHAIN 28 340
 FT TOPO_DOM 28 226
 FT TRANSMEM 227 247
 FT TOPO_DOM 248 340
 FT MOTIF 338 340
 FT CARBOHYD 210 210
 FT DISULFID 62 104
 FT DISULFID 92 156
 FT VARIANT 166 166
 FT VARIANT 166 166
 FT R->Q.
 FT /FTID=VAR_002356.
 SEQUENCE 340 AA; 35835 MW; 5EDF2A32C2FDE79F CRC64;

Query Match 100.0%; Score 1850; DB 1; Length 340;
 Best Local Similarity 100.0%; Pred. No. 3.9e-111;
 Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGPPSHGPGGVVAGLLLLGLVGLVSGLSLEPVYNNANKRFQAGGYLVLPQIGRDL 60
 DB 1 MGPPSHGPGGVVAGLLLLGLVGLVSGLSLEPVYNNANKRFQAGGYLVLPQIGRDL 60
 QY 61 LCPRARPPGPHSSPNVEFYKYLTVGAQGRRCRAPAPNLLTCDRPDLLRFTIKQGY 120
 DB 61 LCPRARPPGPHSSPNVEFYKYLTVGAQGRRCRAPAPNLLTCDRPDLLRFTIKQGY 120
 QY 121 SPNLWGHERRSHHDYIITATSDCTREGLESLOGGYCLTGMVLLRVGSGPGGAVPRKP 180
 DB 121 SPNLWGHERRSHHDYIITATSDCTREGLESLOGGYCLTGMVLLRVGSGPGGAVPRKP 180
 QY 181 VSEMPMERDGAHSLPEKENTLPGDPTSNATSRGEGPLPPSPMPVAVGAAGLALLL 240
 DB 181 VSEMPMERDGAHSLPEKENTLPGDPTSNATSRGEGPLPPSPMPVAVGAAGLALLL 240
 QY 241 GVAAGAGAMCWRRRRAKPSRRHPGSGFRGSGSLGLGGGGMGPRAEPGEIGIALRGG 300
 DB 241 GVAAGAGAMCWRRRRAKPSRRHPGSGFRGSGSLGLGGGGMGPRAEPGEIGIALRGG 300
 QY 301 GAADPPFCPHYKVGSDYGHPIYIVQDPPGPPNITYYV 340
 DB 301 GAADPPFCPHYKVGSDYGHPIYIVQDPPGPPNITYYV 340
 RESULT 2
 EFNB3 MOUSE STANDARD; PRT; 340 AA.
 AC 035393;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 10-MAY-2003 (Rel. 47, Last annotation update)
 DE Ephrin-B3 precursor.
 GN Name=Efnb3;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 ON NCB1_TaxID=10090;
 RX NCBI_TaxID=10090;
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=98143367; PubMed=9484836; DOI=10.1038/94.0nc.1201557;
 RA Bergemann A.D., Zhang L., Chiang M.-K., Brambilla R., Klein R.,
 RA Flanagan J.G.,
 RT "Ephrin-B3, a ligand for the receptor EphB3, expressed at the midline
 RT of the developing neural tube.";
 RL Oncogene 16:471-480(1998).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Klausner R.D., Collins F.S., Wagner L., Shennen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshynski S., Carninci P., Prange C.,
 RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mollath S.J.,
 RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S.C., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield V.S.N., Krzywincki M.I., Skalska U., Smalins D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP FUNCTION.
 RX MEDLINE=20171264; PubMed=10704386;
 RA Imondal R., Wildeman C., Kaprielian Z.;
 RT "Complementary expression of transmembrane ephrins and their receptors
 in the mouse spinal cord: a possible role in constraining the
 RT orientation of longitudinally projecting axons.";
 RL Development 127:1397-1410(2000).
 CC -1- FUNCTION: May play a pivotal role in forebrain function. Binds to,
 CC and induce the collapse of, commissural axons/growth cones in
 CC vitro. May play a role in constraining the orientation of
 CC longitudinally projecting axons.
 CC -1- SUBUNIT: Interacts with GRIP1 and GRIP2 (by similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: Expressed on lateral floor plate cells,
 CC specifically on commissural axon segments that have passed through
 CC the floor plate. Expressed in cells of the retinal ganglion cell
 CC layer during retinal axon guidance to the optic disk.
 CC -1- DEVELOPMENTAL STAGE: Expressed in the floor plate throughout the
 CC period of commissural axon pathfinding.
 CC -1- SIMILARITY: Belongs to the ephrin family.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL; AF025288; AAC53537.1; -; mRNA.
 CC EMBL; BC052001; AAH52001.1; -; mRNA.
 CC EMBL; BC058617; AAH58617.1; -; mRNA.
 CC HSSP; P52800; IIKO.
 CC Ensemble; ENSMUSG0000003934; Mus musculus.
 CC DR MGI; MGI:109196; Efnb3.
 CC DR GO; GO:0005615; C:extracellular space; TAS.
 CC DR GO; GO:0016021; C:integral to membrane; TAS.
 CC DR GO; GO:0007628; P:adult walking behavior; IMP.
 CC DR GO; GO:0016198; P:axon choice point recognition; IMP.
 CC DR InterPro; IPR001799; Ephrin.
 CC DR Pfam; PF00812; Ephrin; 1.
 CC DR PRINTS; PR01347; EPHRIN.
 CC DR ProDom; PD002533; Ephrin; 1.
 CC DR PROSITE; PS01299; EPHRIN; 1.
 CC KW Developmental protein; Differentiation; Glycoprotein; Neurogenesis;
 CC Signal; Transmembrane.
 CC FT SIGNAL 1 27 Potential.
 CC FT CHAIN 28 340 Ephrin-B3.
 CC FT TOPO_DOM 28 327 Extracellular (Potential).
 CC FT TRANSMEM 228 248 Potential.
 CC FT TOPO_DOM 249 340 Cytoplasmic (Potential).
 CC FT MOTIF 338 340 PDZ recognition motif (Potential).
 CC FT CARBOHYD 210 210 N-linked (GlcNAc...) (Potential).
 CC FT DISUFID 62 104 By similarity.
 CC FT DISUFID 92 156 By similarity.
 CC SQ SEQUENCE 340 AA; 35885 MW; 52F3D58FD209A6B8 CRC64;
 CC
 CC Query Match 96.2%; Score 1780; DB 1; Length 340;
 CC Best Local Similarity 95.6%; Pred. No. 1,2e-106;
 CC Matches 325; Conservative 7; Mismatches 8; Indels 0; Gaps 0;
 CC
 CC QY 1 MGPHSGGSGVAVGALLGLVGLVSGLSLEPYWNSANTRFOAEGGYLYPOIGDRDL 60
 CC DB 1 MGAPHPGPGGVGVGALLGLFAGLVSGLSLEPYWNSANTRFOAEGGYLYPOIGDRDL 60
 CC QY 61 LCPRARPGGHSSPNTVEFYLYVGAGGRCAPAPVNLITCDPRDLARTIKROEY 120
 CC DB 61 LCPRARPGGHSSPNTVEFYLYVGAGGRCAPAPVNLITCDPRDLARTIKROEY 120
 CC QY 121 SPNLMGHEFRSHHDYIATSDGTREGLSLOGVCLTRGMKYLRLVGSGPRGAVPRKP 180
 CC DB 121 SPNLMGHEFRSHHDYIATSDGTREGLSLOGVCLTRGMKYLRLVGSGPRGAVPRKP 180

DB 121 SPNLMGHEFRSHHDYIATSDGTREGLSLOGVCLTRGMKYLRLVGSGPRGAVPRKP 180
 QY 181 VSEMPERDRGAHSLPEKGNLPDPTSNATSRGAEGLPPSPMPAVAGAAGLALL 240
 DB 181 VSEMPERDRGAHSLPEKGNLPDPTSNATSRGAEGLPPSPMPAVAGAAGLALL 240
 QY 241 GVAGAGCAGCWRRRRAKPSERRHPGSGFGGSLGLGGGCGMPREAEDEIGIALRG 300
 DB 241 GVAGAGCAGCWRRRRAKPSERRHPGSGFGGSLGLGGGCGMPREAEDEIGIALRG 300
 QY 301 GAADPPCPHYEKVSGDYGHPIYTVODGPPQSPNITYRV 340
 DB 301 GTADPPCPHYEKVSGDYGHPIYTVODGPPQSPNITYRV 340
 CC
 CC RESULT 3
 CC Q5F221.MOUSE
 CC ID Q5F221.MOUSE PRELIMINARY; PRT; 340 AA.
 CC AC Q5F221;
 CC DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 CC DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 CC DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 CC DE Ephrin B3 (16 days embryo head cDNA, RIKEN full-length enriched
 CC library, clone:Cl30048B01 product:m-ephrin-B3).
 CC GN Name=Efnb3; ORFNames=RP23-56120.5-001;
 CC OS Mus musculus (Mouse).
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC OC Mammalia; Eutheria; Barchontoglires; Glires; Rodentia; Sciurognathi;
 CC OC Muridae; Murinae; Mus.
 CC OX NCBI_TaxId=10090;
 CC RN [1]
 CC RP NUCLEOTIDE SEQUENCE.
 CC RA Tromans A.;
 CC RL Submitted (FEF-2005) to the EMBL/GenBank/DBJ databases.
 CC RN [2]
 CC RP NUCLEOTIDE SEQUENCE.
 CC RC STRAIN=C57BL/6J; TISSUE=Head;
 CC RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99) 03004-9;
 CC RA Carninci P., Hayashizaki Y.;
 CC RT "High-efficiency full-length cDNA cloning.";
 CC RL Meth. Enzymol. 303:19-44(1999).
 CC RN [3]
 CC RP NUCLEOTIDE SEQUENCE.
 CC RC STRAIN=C57BL/6J; TISSUE=Head;
 CC RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 CC RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 CC RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 CC RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
 CC RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 CC RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 CC RA Fleischmann W., Gaasterland T., Giesi C., King B., Kochiwa H.,
 CC RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 CC RA Schirml L.M., Staudl F., Suzuki R., Tomita M., Wagner L., Washio T.,
 CC RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Bash G.,
 CC RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 CC RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 CC RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 CC RA Lyons P., Marchionni L., Mashima J., Mazarrelli U., Mombarts P.,
 CC RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 CC RA Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F.,
 CC RA Suzuki H., Toyokawa K., Wang K.H., Weitz C., Whitlaker C., Wilmshurst T.,
 CC RA Wyszynski B., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
 CC RA Hayashizaki Y.;
 CC RT "Functional annotation of a full-length mouse cDNA collection.";
 CC RL Nature 409:685-690(2001).
 CC RN [4]
 CC RP NUCLEOTIDE SEQUENCE.
 CC RC STRAIN=C57BL/6J; TISSUE=Head;
 CC RX MEDLINE=22354683; PubMed=1246851; DOI=10.1038/nature01266;
 CC RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 CC RA Nikaide I., Otsu N., Saito R., Suzuki H., Yamataka I., Kiyosawa H.,
 CC RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schoenbach C., Gojobori T.,
 CC RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

RA Schirnl L.M., Knapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Bruscia V., Chochia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gibsi C., Godzik A., Gough J.,
RA Grimmerd S., Guelinckx S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., Kling B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Matsats L., Marchionni L., McKenlie L., Miki H.,
RA Nagashima T., Nunnata K., Okido T., Pavan W.J., Petrea G., Peeole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sanderlin A., Schneider C., Semple C.A., Secou M., Shimada K.,
RA Sultana R., Tanaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wyszynski-Boris A., Yangisawa M., Yang J., Yang L.,
RA Yuan Z., Zavalon M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-fukushima T., Kono H., Nakamura M., Sakazume N., Sato K.,
RA Shiraiki T., Waki K., Kawai J., Aizawa K., Arahata T., Fukuda S.,
RA Hara A., Hashizume W., Imocani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yaeunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.,
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs";
RL Nature 420:563-573(2002).
[5]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Head;
RC MEDLINE=20499374; PubMed=11024159; DOI=10.1101/gr.145100;
RX Shiba K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Kono H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara B., Watanaki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai Y.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer";
RL Genome Res. 10:1757-1771(2000).
[7]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Head;
RC Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imocani K., Ishii Y., Itoh M., Kagawa I., Kaubawa T.,
RA Kachi H., Kawai Y., Kojima Y., Kondo S., Kono H., Koya S.,
RA Kurihara C., Matsumura T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohnishi N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraiki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toyota T., Yaeunishi A., Muramatsu M., Hayashizaki Y.,
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL, AL731687; CAIS2012.1; -; Genomic_DNA.
DR EMBL, AK048305; BAC33229.1; -; mRNA.
SQ SEQUENCE 340 AA; 35884 MW; 52F3D58FDF209A688 CRC64;
Query Match 96.2%; Score 1780; DB 2; Length 340;
Best Local Similarity 95.6%; Pred. No. 1,2e-106;
Matches 325; Conservative 7; Mismatches 8; Indels 0; Gaps 0;
1 MGPHISGGVAVGALLLIGLVGVSLEBTVNNSANKRFOAGSGVTVLPQIGRDL 60

Db	1	MGAFHFGGVGVQVGVALLLLGAGLVSGLSLEPVTWNSANKRFQAEGGVYLYPQIGDRDLT	60
Oy	61	LCPPARPGRPSSSNVPEFYKLYLVGAGQGRCEAPPAENLLLTCDRPLDRLFTTKFOEY	120
Db	61	LCPPARPGRPSSSNVPEFYKLYLVGAGQGRCEAPPAENLLLTCDRPLDRLFTTKFOEY	120
Oy	121	SPNLMGHEFRSHHHYIIATSDGTREGLESIGQGVCLTRGKVVLLRVQSPDRGAVPRKP	180
Db	121	SPNLMGHEFRSHHHYIIATSDGTREGLESIGQGVCLTRGKVVLLRVQSPDRGAVPRKP	180
Oy	181	VSEMPMERDRGAHSLEPGKENLPGDPTSNATSHGAEGLPPBSPMPAVAGAAGLALLL	240
Db	181	VSEMPMERDRGAHSLEPGKENLPGDPTSNATSHGAEGLPPBSPMPAVAGAAGLALLL	240
Oy	241	GVAAGAGCMCKRRRRARPSESRHNGPSPGFCGSLGICGGCGMPREAPPELGIALRG	300
Db	241	GVAAGAGCMCKRRRRARPSESRHNGPSPGFCGSLGICGGCGMPREAPPELGIALRG	300
Oy	301	GAADPFCPPHYEKVSGDYGHVPVTVVOGPPSPPNIIYKVV 340	
Db	301	GTADPPFCPPHYEKVSGDYGHVPVTVVOGPPSPPNIIYKVV 340	
RESULT 4			
O90Z31_BRARE PRELIMINARY; PRT; 331 AA.			
ID	O90Z31_	BRARE PRELIMINARY;	PRT; 331 AA.
AC	O90Z31;		
DT	01-DEC-2001	(TREMBlrel. 19, Created)	
DT	01-DEC-2001	(TREMBlrel. 19, Last sequence update)	
DT	01-OCT-2003	(TREMBlrel. 25, Last annotation update)	
DE	Ephrin B3.		
GN	Name=efnb3;		
OS	Brschydantio rerio (Zebrafish) (Danio rerio).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;		
OC	Cyprinidae; Danio.		
OX	NCBI_TaxId=7955;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RX	MEDLINE=21290827; PubMed=11397014; DOI=10.1006/dbio.2001.0281;		
RA	Chan J., Mabry J.D., Serluca F.C., Chen J.N., Goldstein N.B.,		
RA	Thomas M.C., Cleary J.A., Brennan C., Fishman M.C., Roberts T.M.;		
RT	"Morphogenesis of prechordal plate and notochord requires intact		
RT	epn/ephrin b signaling."		
RL	Dev. Biol. 224:470-482(2001).		
DR	EMBL; AF375227; AAK64277.1; -; mRNA.		
DR	HSSep; P52800; iIKO.		
DR	Ensembl; ENSDARG000008177; Danio rerio.		
DR	ZFIN; ZDB-GENE-010618-3; efnb3.		
DR	GO; GO:0016020; C:membrane; IEA.		
DR	InterPro; IPR001799; Ephrin.		
DR	Pfam; PF00812; Ephrin.1.		
DR	PRINTS; PR01347; EPHRIN.		
DR	Prodom; PD002533; Ephrin.1.		
DR	PROSITE; PS01299; EPHRIN; 1.		
SQ	SEQUENCE 331 AA; 35638 MW; 6A5EACD509A09818 CRC64;		
Query Match 49.9%; Score 923; DB 2; Length 331;			
Best Local Similarity 54.8%; Pred. No. 1.5e-51;			
Matches 190; Conservative 43; Mismatches 74; Indels 40; Gaps 10;			
Db	9	GLGIILFLVLDLGL-ITATNMEPIYWNLSLNGKFSDDKGYLYVYPOIGDRDLTICPSSDPDG	67
Oy	10	GVRVGVALLLLGVGLVSGLSLEPVTWNSANKRFQAEGGVYLYPQIGDRDLTICPPARPDG	69
Db	9	GLGIILFLVLDLGL-ITATNMEPIYWNLSLNGKFSDDKGYLYVYPOIGDRDLTICPSSDPDG	67
Oy	70	PHSSPNTVEFYKLYLVG-AGGRCEAPPAENLLLTCDRPLDRLFTTKFOEYSPNLMGHE	128
Db	68	PRADADVEYKLYLVSSREQADRECVTGAPNLLLTCDKPKNSDMFTTKFOEYSPNLMGHE	127
Oy	129	FRSHHDYIIATSDGTREGLESIGQGVCLTRGKVVLLRVQSPDRG- GAVPRKPVSEME	187
Db	128	FKTHHDYIIATSDGTREGLESIMRGVCATGKVVLLRVQSPFYGLPAKSKFPDS-----	182

QY 188 RDRGAHSLPEPKENLPGDPTSNAT-----SRGAEGLPPSPMPAVAGAAGLALL 239
 DB 183 -----AGRINPNPCTGNSTHPQIPRPGSGGENGLPASNIAVAGAAGSAPFL 232
 QY 240 LGVAGAGAMCWMRRRAKPSSESRHPGSGFG-----RGSLGLGGGGGMPREABEGL 293
 DB 233 L-VTAVICVVCYRRRAKSHSESHRP-PLSLSLTSPKRCGGCGVGCGNNNG---SEPSDI 287
 QY 294 GIALRGGAADPPFCPHYEKVSGDYGHPIYVODGPPSPENITYKY 340
 DB 288 IIFLR---TSDSAVCPHYEKVSGDYGHPIYVODGPPSPENITYKY 331

RESULT 5

050203 BRARE
 ID 050203 BRARE PRELIMINARY; PRT; 342 AA.
 AC 050203;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Fmb3 protein.
 GN Name:fmb3;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 NC NCBI_TaxId=7955;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins B.S., Wagner K.H., Shenmen C.M., Schlier G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Hsieh F.,
 RA Diatchenko L., Marulanda K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stacheron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Tomshyuk S., Carninci P., Mullaney S.J.,
 RA Raha S.S., Loughlano N.A., Peters G.J., Abramson R.D., Millaby S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richardson S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Murray D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahney J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Rutherford J.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Brain;
 RG NIH MGC Project;
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
 SQ EMBL; BC095605; AAH95605.1; -; mRNA.
 SQ SEQUENCE 342 AA; 36885 MW; 1629532234F85386 CRC64;

Query Match 49.9%; Score 923; DB 2; Length 342;
 Best Local Similarity 54.8%; Pred. No. 1.6e-51;
 Matches 190; Conservative 43; Mismatches 74; Indels 40; Gaps 10;

QY 10 GYRVALLLLGLVGLVSLSPVYNNANKRFQAGGYLYVQIGDRDLDCPRAPPG 69
 DB 20 GGIILIFIVDLIG-ITATNMEPIYNNNSNKRPSDKGYLYVQIGDRDLDCPSDPPG 78
 QY 70 PHSSPYEYKYLYLVGG-AQGRCEAPPAENLLITCDRDLDFRTIKFOESPNLMGHE 128
 DB 79 PAAPADYETKYLYLVSSREQADRCETGAPNLLITCDKPSDKRFTIKFOESPNLMGHE 138
 QY 129 FSSHHDYIATSDGTREGLESLOGGVCLTRGMKVLRLVQSGSPRG-GAVPRKRVSEMPME 187
 DB 129 FSSHHDYIATSDGTREGLESLOGGVCLTRGMKVLRLVQSGSPRG-GAVPRKRVSEMPME 187

DB 139 FKTNDHYFIATSDGTREGLESNRGVCATQGMKVLKVQSGPYGLPAKSPKDS----- 193
 QY 188 RDRGAHSLPEPKENLPGDPTSNAT-----SRGAEGLPPSPMPAVAGAAGLALL 239
 DB 194 -----AGRINPNPCTGNSTHPQIPRPGSGGENGLPASNIAVAGAAGSAPFL 243
 QY 240 LGVAGAGAMCWMRRRAKPSSESRHPGSGFG-----RGSLGLGGGGGMPREABEGL 293
 DB 244 L-VTAVICVVCYRRRAKSHSESHRP-PLSLSLTSPKRCGGCGVGCGNNNG---SEPSDI 298
 QY 294 GIALRGGAADPPFCPHYEKVSGDYGHPIYVODGPPSPENITYKY 340
 DB 299 IIFLR---TSDSAVCPHYEKVSGDYGHPIYVODGPPSPENITYKY 342

RESULT 6

09PT69 XENLA
 ID 09PT69 XENLA PRELIMINARY; PRT; 327 AA.
 AC 09PT69;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Ephrin-B3 precursor.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
 OC Xenopodinae; Xenopus; Xenopus.
 NC NCBI_TaxId=8355;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Embryonic head;
 RX MEDLINE=20096673; PubMed=10633856;
 RX DOI=10.1002/(SICI)1097-0177(199912)216:4/5<361::AID-DVUY53.0.CO;2-W;
 RA Helbling P.M., Saulnier D.M.E., Robinson V., Christiansen J.H.,
 RA Wilkison D.G., Brandt A.W.,
 RT "Comparative analysis of embryonic gene expression defines potential
 interaction sites for Xenopus EphA4 receptors with ephrin-B ligands";
 RL Dev. Dyn. 216:361-373(1999).
 DR EMBL; AJ236866; CAB65511.1; -; mRNA.
 DR HSP; P52800; I1KO.
 DR GO; GO:0016020; C:membrane, IEA.
 DR InterPro; IPR002086; Aldehyd_dehydrotog.
 DR InterPro; IPR001799; Ephrin.
 DR Pfam; PF006812; Ephrin; 1.
 DR PRINTS; PR01347; EPHRIN.
 DR ProDom; PD002533; Ephrin; 1.
 DR PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; UNKNOWN_1.
 DR PROSITE; PS01299; EPHRIN; 1.
 KM Signal.
 FT SIGNAL.
 SQ SEQUENCE 327 AA; 35913 MW; 4BB0FA39D4C22DDC CRC64;

Query Match 49.7%; Score 919; DB 2; Length 327;
 Best Local Similarity 60.4%; Pred. No. 2.7e-51;
 Matches 192; Conservative 30; Mismatches 82; Indels 14; Gaps 8;

QY 25 VGLSLSPVYNNANKRFQAGGYLYVQIGDRDLDCPRAPPGHSPNTEFYKLYV 84
 DB 22 ISALSLDPIYNNNSNKRPFEDTGGVLYVQIGDRDLDCPSBPQGFSSPYEYKLYV 81
 QY 85 GGAOG-RRCCEAPPAENLLITCDRDLDFRTIKFOESPNLMGHEFSSHHDYIATSDG 143
 DB 82 GTEKEMSSCSILRTNLLITCDRDLDFRTIKFOESPNLMGHEFSGRDYIATSDG 141
 QY 144 TREGLESLOGGVCLTRGMKVLRLVQSGSPRGAVPRKRVSEMPERDGAHSL-EPGKEN 202
 DB 142 TMDGIETIQGVCEITKGMKVTLLKVGQSPNAPPRPSS---AGKDSGISPVNPDLPN 198
 QY 203 LRGDPSNATSGAGAPPAENLLITCDRDLDFRTIKFOESPNLMGHEFSSHHDYIATSDG 262
 DB 199 V-GETSGNATKTGNGENPPIHVPLVAGAAGLALLL-VFVVVAVVCHRRQAGHSDTR 256
 QY 263 HPGPSFGKGSGLGCGGGMGPREABEGLIALRGGAADPPFCPHYEKVSGDYGHV 322

DB 257 HB-PLISGITSBPKRGNN-----NGHEPBDIIMPLRPSEAG-AFCPHYKXSGDGHFV 309
 QY 323 YIVODSPSPNNIYKYV 340
 DB 310 YIVODMASOSPANNIYKYV 327

RESULT 7
 EPNB2 MOUSE
 ID EPNB2 MOUSE STANDARD; RRT; 336 AA.
 AC P52800;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Ephrin-A2 precursor (EPH-related receptor tyrosine kinase ligand 5) (LEK-5) (HTK ligand) (HTK-L) (ELF-2).
 GN Name=Elf2; Synonyms=Elf2, Epl5, Epl95, Hck1, Lerk5;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murine; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=96145238; PubMed=8559144; DOI=10.1016/0161-5890(95)00108-5;
 RA Cerretti D.P., Vanden Boes T., Nelson N., Kozlosky C.J., Reddy P.,
 RA Maraskovsky E., Park L.S., Lyman S.D., Copeland N.G., Gilbert D.J.,
 RA Jenkins N.A., Fletcher R.A.;
 RT "Isolation of LEK-5: a ligand of the eph-related receptor tyrosine
 RT kinases.";
 RL Mol. Immunol. 32:1197-1205(1995).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RX STRAIN=CB57BL/6J X SUI/J;
 RX MEDLINE=95199254; PubMed=7534404;
 RA Bennett B.D., Zeigler F.C., Gu Q., Fendly B., Goddard A.D.,
 RA Gillett N., Matthews W.;
 RT "Molecular cloning of a ligand for the EPH-related receptor protein-
 RT tyrosine kinase Hck.";
 RL Proc. Natl. Acad. Sci. U.S.A. 92:1866-1870(1995).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RX STRAIN=ICR; TISSUE=Brain;
 RX MEDLINE=95379837; PubMed=7651410;
 RA Klausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins E., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hecht F.,
 RA Diachenko L., Marinina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Brownstein M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mallya S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huijck S.W.,
 RA Villalon D.K., Muray D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahney U., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield V.S.N., Krzywicki M.I., Skalska U., Smalls D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:1699-16903(2002).
 RN [5]
 RP FUNCTION.
 RX MEDLINE=20171264; PubMed=10704386;
 RA Imondi R., Wideman C., Kaprielian Z.;
 RT "Complementary expression of transmembrane ephrins and their receptors
 RT in the mouse spinal cord: a possible role in constraining the
 RT orientation of longitudinally projecting axons.";
 RL Development 127:1397-1410(2000).
 RN [6]
 RP X-RAY CRYSTALLOGRAPHY (1.92 ANGSTROMS) OF 30-170.
 RX PubMed=11703926; DOI=10.1016/S1534-5807(01)00002-8;
 RA Toch J., Cutforth T., Gellinas A.D., Bethoney K.A., Bard J.,
 RA Harrison C.J.;
 RT "Crystal structure of an ephrin ectodomain.";
 RL Dev. Cell 1:83-92(2001).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 31-168 IN COMPLEX WITH EPNB2.
 RX PubMed=11780069; DOI=10.1038/414933a;
 RA Himanen J.-P., Rajashankar K.R., Lackmann M., Cowan C.A.,
 RA Henkemeyer M., Nikolov D.B.;
 RT "Crystal structure of an Eph receptor-ephrin complex.";
 RL Nature 414:933-938(2001).
 CC -1- FUNCTION: Binds to the receptor tyrosine kinases EPNB2 and EPNB4.
 CC May play a role in constraining the orientation of longitudinally
 CC projecting axons.
 CC -1- SUBUNIT: Interacts with PDZRN3 (by similarity). Binds to the
 CC receptor tyrosine kinase EPNB4.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: Expressed on lateral floor plate cells,
 CC specifically on commissural axon segments that have passed through
 CC the floor plate. Expressed in cells of the retinal ganglion cell
 CC layer during retinal axon guidance in the floor plate throughout the
 CC -1- DEVELOPMENTAL STAGE: Expressed in the floor plate throughout the
 CC -1- PFM: Inducible phosphorylation of tyrosine residues in the
 CC cytoplasmic domain (by similarity).
 CC -1- SIMILARITY: Belongs to the ephrin family.
 CC
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC
 CC EMBL; U16819; AAA9708.1; -; mRNA.
 CC EMBL; U38847; AAC42052.1; -; mRNA.
 CC EMBL; U30244; AAA82934.1; -; mRNA.
 CC EMBL; BC057009; AAH57009.1; -; mRNA.
 CC PIR; I49766; I49766.
 CC PDB; 1IKO; X-ray; P=30-207.
 CC PDB; 1KGY; X-ray; E/F/G/H=31-168.
 CC Ensembl; ENSMUSG0000001300; Mus musculus.
 CC MGI; MGI:105097; Efnb2.
 CC GO; GO:0005615; C:cytoskeleton; TAS.
 CC GO; GO:0016021; C:integral to membrane; TAS.
 CC GO; GO:0005886; C:plasma membrane; IDA.
 CC GO; GO:0005515; F:protein binding; IDA.
 CC GO; GO:0001945; P:lymph vessel development; IMP.
 CC GO; GO:0009887; P:organogenesis; IMP.
 CC InterPro; IPR001799; Ephrin.
 CC Pfam; PF00812; Ephrin_1.
 CC PRINTS; PR01347; EPHRIN.
 CC ProDom; PD002533; Ephrin_1.
 CC PROSITE; PS01299; EPHRIN_1.
 CC 3D-structure; Developmental protein; Differentiation; Glycoprotein;
 CC Neurogenesis; Phosphorylation; Signal; Transmembrane.
 CC SIGNA1; 1; 28
 CC CHAIN; 29; 336
 CC TOPO_DOM; 29; 232
 CC TRANSMEM; 233; 253
 CC TOPO_DOM; 254; 336
 CC MOTIF; 334; 336
 CC PDZ recognition motif (Potential).

FT CARBOHYD 39 39 N-linked (GlcNAc...),
 FT CARBOHYD 142 142 N-linked (GlcNAc...), (Potential).
 FT DISULFID 65 104
 FT DISULFID 92 156
 FT CONFLICT 3 4 Missing (in Ref. 3).
 FT CONFLICT 177 177 A -> T (in Ref. 1).
 FT STRAND 36 37
 FT TURN 40 41
 FT TURN 43 44
 FT TURN 46 46
 FT TURN 47 49
 FT TURN 50 52
 FT TURN 57 58
 FT STRAND 60 65
 FT STRAND 72 73
 FT STRAND 79 84
 FT HELIX 86 90
 FT TURN 91 92
 FT STRAND 93 93
 FT STRAND 99 104
 FT TURN 107 108
 FT STRAND 111 116
 FT TURN 124 125
 FT TURN 131 132
 FT STRAND 134 139
 FT HELIX 145 147
 FT TURN 148 149
 FT STRAND 152 152
 FT TURN 154 154
 FT HELIX 155 158
 FT STRAND 162 162
 SQ SEQUENCE 336 AA; 37202 MW; D08894996B399554 CRC64;

Query Match 34.5%; Score 637.5; DB 1; Length 336;
 Best Local Similarity 42.1%; Pred. No. 3.5e-33;
 Matches 139; Conservative 49; Mismatches 129; Indels 13; Gaps 5;

QY 14 GALLLGLVGLVSGLEPYNNANKRFOAEGYVLPQIGRDLDCRRARPDPHSS 73
 DB 17 GLIMVLCRTAISRISVLEPYNNSSKFLPGQGLVLPQIGDKLIDCPKV--DSKTV 73
 QY 74 PNYEFKYLIVGAGORCEAPPAENLLTCRPRDLDRFTIKFOEYSPYLMGHEFRSHH 133
 DB 74 GQYEVYKVMVNDQADRCTIKKENTPLNLCARPDDVFTIKFOEFSPLYLWGLEFQKK 133
 QY 134 DYYIATSGTRGEGSLGGVCLTRGMKYLKRVG--SPRGAVPRKPYSEMPMER-DR 190
 DB 134 DYYIISTSGSLGELNDEGVQCOTRAMKILMKVGDASAGSARHNGPTRRPELEAGTN 193
 QY 191 GAHSLPEPKENLPDPTSNATSRGAEGPLPPSPMPAVNAGAGLALLLVAGAGAGMC 250
 DB 194 GRSSTSPVYKPNPGSGSTGNSAGHGNLLGSEVALPFGIAGGCIIFITITLVLL 253
 QY 251 WRRRAKPEBSRHPGSGFRGSGSLGLGGCGGMPREAREGELALRGAGADPPFCRH 310
 DB 254 KYRRRRRKHSPOHTTLLSLSTLATPRKGGNN----NGSEPSDVIPLR---TADSVFCRH 306
 QY 311 YEKVSGDYGHPPYIVDDGPPSPNITYYK 340
 DB 307 YEKVSGDYGHPPYIVDEMPQSPANIYYK 336

RESULT 8
 Q4FJM3_MOUSE PRELIMINARY; PRT; 336 AA.
 AC Q4FJM3;
 DT 13-SEP-2005 (TEMBLrel. 31, Created)
 DT 13-SEP-2005 (TEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TEMBLrel. 31, Last annotation update)
 DE Efnb2 protein.
 GN Name=Efnb2;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muroidae; Muridae; Murinae; Mus.
 OC NCBI_TaxId=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Ebert L., Muenstermann E., Schatten R., Henze S., Bohn E.,
 RA Mollenhauer J., Wiemann S., Schick M., Korn B.,
 RT "Cloning of mouse full open reading frames in Gateway(R) system entry
 RT vector (pDONR201).";
 RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; CTO10381; CAD18588.1; -; mRNA.
 SQ SEQUENCE 336 AA; 37202 MW; D08894996B399554 CRC64;

Query Match 34.5%; Score 637.5; DB 2; Length 336;
 Best Local Similarity 42.1%; Pred. No. 3.5e-33;
 Matches 139; Conservative 49; Mismatches 129; Indels 13; Gaps 5;

QY 14 GALLLGLVGLVSGLEPYNNANKRFOAEGYVLPQIGRDLDCRRARPDPHSS 73
 DB 17 GLIMVLCRTAISRISVLEPYNNSSKFLPGQGLVLPQIGDKLIDCPKV--DSKTV 73
 QY 74 PNYEFKYLIVGAGORCEAPPAENLLTCRPRDLDRFTIKFOEYSPYLMGHEFRSHH 133
 DB 74 GQYEVYKVMVNDQADRCTIKKENTPLNLCARPDDVFTIKFOEFSPLYLWGLEFQKK 133
 QY 134 DYYIATSGTRGEGSLGGVCLTRGMKYLKRVG--SPRGAVPRKPYSEMPMER-DR 190
 DB 134 DYYIISTSGSLGELNDEGVQCOTRAMKILMKVGDASAGSARHNGPTRRPELEAGTN 193
 QY 191 GAHSLPEPKENLPDPTSNATSRGAEGPLPPSPMPAVNAGAGLALLLVAGAGAGMC 250
 DB 194 GRSSTSPVYKPNPGSGSTGNSAGHGNLLGSEVALPFGIAGGCIIFITITLVLL 253
 QY 251 WRRRAKPEBSRHPGSGFRGSGSLGLGGCGGMPREAREGELALRGAGADPPFCRH 310
 DB 254 KYRRRRRKHSPOHTTLLSLSTLATPRKGGNN----NGSEPSDVIPLR---TADSVFCRH 306
 QY 311 YEKVSGDYGHPPYIVDDGPPSPNITYYK 340
 DB 307 YEKVSGDYGHPPYIVDEMPQSPANIYYK 336

RESULT 9
 EFNBL_HUMAN STANDARD; PRT; 346 AA.
 AC P98172;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Ephrin-B1 precursor (EPH-related receptor tyrosine kinase ligand 2)
 DE (LRRK-2) (Euk-L).
 GN Name=Efnb1; Synonyms=BFL-3, EPLG2, LRRK2;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
 OC Homo.
 OC NCBI_TaxId=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Placenta;
 RX MEDLINE=94349923; PubMed=8070404;
 RA Beckmann M.P., Cerrretti D.P., Baum P., Vanden Bos T., James L.,
 RA Fretschel T., Kozlowsky C., Hollingsworth T., Shilling H., Maraskovsky E.,
 RA Fletcher F.A., Lhotak V., Pawson T., Lyman S.D.,
 RT "Molecular characterization of a family of ligands for eph-related
 RT tyrosine kinase receptors";
 RL EMBO J. 13:3757-3762(1994).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=95063919; PubMed=7973638;
 RA Davis S., Gale N.W., Aldrich T.H., Maisompierre P.C., Lhotak V.,
 RA Pawson T., Goldfarb M., Yancopoulos G.D.,
 RT "Ligands for EPH-related receptor tyrosine kinases that require

membrane attachment or clustering for activity.";
RL Science 266:816-819(1994).
RN (3)
RA NUCLEOTIDE SEQUENCE.
RP Fletcher F.A., Hubbard K., Shaffer L.G., Monaco A., Mueller U.,
RA Kozlosky C., Duck T., Simoneaux D.K., Fairweather N., Chelly J.,
RA Czeretli D.P., Belmont J.W., Beckmann M.P., Lyman S.D.;
RT "Assignment of the human Elk1 gene, EPG2, to chromosome region
Xq12.";
RT Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RA NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15772651; DOI=10.1038/nature03440;
RA Ross M.T., Graham D.V., Coffey A.J., Scherer S., McLay K., Muzny D.,
RA Platter M., Howell G.R., Burrows C., Bird C.P., Frankish A.,
RA Lovell F.L., Howe K.L., Ashurst J.L., Fulton R.S., Sudrak R., Wen G.,
RA Jones M.C., Hultes M.E., Andrews T.D., Scott C.E., Sealie S.,
RA Rameer J., Whitaker A., Deadman R., Carter N.P., Hunt S.E., Chen R.,
RA Cree A., Gunaratne P., Havlik P., Hodgson A., Metzger M.L.,
RA Richards S., Scott G., Steffen D., Sodergren E., Wheeler D.A.,
RA Worley K.C., Alencough R., Ambrose K.D., Ansari-Lari M.A., Aradhy S.,
RA Ashwell R.I., Babbage A.K., Baguley C.L., Ballabio A., Banerjee R.,
RA Barker G.E., Barlow K.F., Barrett I.P., Bates K.N., Beare D.M.,
RA Beasley H., Beasley O., Beck A., Bethel G., Blechschmidt K., Brady N.,
RA Bray-Allen S., Bridgeman A.M., Brown A.J., Brown M.J., Bonnin D.,
RA Bruford E.A., Buhay C., Burch P., Burford D., Burgess J., Burrill W.,
RA Burton J., Bye J.M., Carder C., Carrel L., Chako J., Chapman J.C.,
RA Chavez D., Chen E., Chen G., Chen Y., Chen Z., Chinault C.,
RA Ciccocioppa A., Clark S.Y., Clarke G., Clee C.M., Clegg S.,
RA Clerc-Blankenburg K., Clifford K., Cobley V., Cole C.G., Conquer J.S.,
RA Corby N., Connor R.E., David R., Davies J., Davis C., Davis J.,
RA Delgado O., Dehazo D., Dharm P., Ding Y., Dinh H., Dodsorth S.,
RA Draper H., Dugan-Hochia S., Dunham A., Dunn M., Durbin K.J., Dutta I.,
RA Eades T., Ellwood M., Emery-Cohen A., Erington H., Evans K.L.,
RA Faulner L., Francis F., Frankland J., Fraser A.E., Galoczzy P.,
RA Gilbert J., Gill R., Gioecker G., Gregory S.G., Gribble S.,
RA Griffiths C., Grocock R., Gu Y., Gwilliam R., Hamilton C., Hart E.A.,
RA Hawes A., Heath P.D., Heilmann K., Hennig S., Hernandez J.,
RA Hinzmann B., Ho S., Hoffe M., Howden P.J., Huckle E.J., Hume J.,
RA Hunt P.J., Hunt A.R., Isherwood J., Jacob L., Johnson D., Jones S.,
RA de Jong P.J., Joseph S.S., Keenan S., Kelly S., Kerhaw J.K., Khan Z.,
RA Klesche P., Klages S., Knights A.J., Kosiura A., Kovar-Smith C.,
RA Laid G.K., Langford C., Lawlor S., Leversha M., Lewis L., Liu W.,
RA Lloyd G., Lloyd D.M., Louisedge H., Loveland J.E., Lovell J.D.,
RA Lozdo R., Lu J., Lyne R., Ma J., Maheshwari M., Matthews L.H.,
RA McDowell J., McLaren S., McWhirley A., Meidl P., Melinger T.,
RA Milne S., Miner G., Mistry S.L., Morgan M., Morris S., Mueller I.,
RA Mullikin J.C., Nguyen N., Nordstiek G., Nyakatura G., O'dell C.N.,
RA Okwono G., Palmer S., Pandian R., Parker D., Parrish J.,
RA Pasternak S., Patel D., Pearce A.V., Pearson D.M., Pelan S.E.,
RA Perez L., Porter K.M., Ramsey Y., Reichwald K., Rhodes S.,
RA Ridler K.A., Schlessinger D., Schuler M.G., Sena H.K.,
RA Shaw-Smith C., Shen H., Sheridan E.M., Showkneen R., Stuce C.D.,
RA Smith M.L., Sothman E.C., Steingruber H.E., Steward C.A., Storey R.,
RA Swann R.M., Swarbreck D., Tabor P.E., Taudien S., Taylor T.,
RA Teague B., Thomas K., Thorpe A., Tims K., Tracey A., Trevanion S.,
RA Tromas A.C., d'Ursio M., Verduzco D., Villasa D., Waldron L.,
RA Wall M., Wang O., Warren J., Warr G.L., Wei X., West A.,
RA Whitehead S.L., Whiteley M.N., Wilkinson J.E., Willey D.L.,
RA Williams G., Williams L., Williamson A., Williamson H., Wilmig L.,
RA Woodmaney R.L., Wray P.W., Yen J., Zhang J., Zhou J., Zoghbi H.,
RA Zorilla S., Buck D., Reinhardt R., Pouster A., Rosenthal A.,
RA Leherich S., Meindl A., Minx P.J., Hillier L.W., Willard H.F.,
RA Wilson R.K., Waterston R.H., Rice C.M., Vaudin N., Coulson A.,
RA Nelson D.L., Waterston G., Sulston J.E., Durbin R., Hubbard T.,
RA Gibbs R.A., Beck S., Rogers J., Bentley D.R.;
RT "The DNA sequence of the human X chromosome.";
RT Nature 434:325-337(2005).
RN [5]
RA NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Eye, and Skin;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Maras M.B., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McMan P.J., McKernan K.D., Malek J.A., Gunaratne P.H.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Faley J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [6]
RA PROTEIN SEQUENCE OF 28-42.
RX PubMed=15340161; DOI=10.1110/ps.04682504;
RA Zhang Z., Hensel W.J.;
RT "Signal peptide prediction based on analysis of experimentally
RT verified cleavage sites.";
RT Protein Sci. 13:2819-2824(2004).
RN [7]
RA INTERACTIONS WITH GRIP1 AND GRIP2.
RC TISSUE=Fetal brain;
RX MEDLINE=99211388; PubMed=10197531; DOI=10.1016/S0896-6273(00)80706-0;
RA Brueckner K., Pablo Labrador J., Scheffele P., Herb A., Seeburg P.H.,
RA Klein R.;
RT "Ephrin ligands recruit GRIP family PDZ adaptor proteins into raft
RT membrane microdomains.";
RT Neuron 22:511-524(1999).
RN [8]
RA VARIANTS CENS LEU-54 AND ILE-111.
RX PubMed=1514102; DOI=10.1086/421532;
RA Wieland I., Jakubiczka S., Muschke P., Cohen M., Thiele H.,
RA Gerlach K.L., Adams R.H., Wleackner P.;
RT "Mutations of the ephrin-B1 gene cause craniofrontonasal syndrome.";
RT Am. J. Hum. Genet. 74:1209-1215(2004).
RN [9]
RA VARIANTS CENS THR-62; SER-98; PRO-115; HIS-119; THR-119; SER-151;
RX VAL-151; PRO-155; ILE-158 AND VAL-158, AND VARIANT HIS-154.
RP PubMed=15166289; DOI=10.1073/pnas.0402819101;
RA Twigg S.R.F., Kan R., Babbs C., Bochkova E.G., Robertson S.P.,
RA Wall S.A., Morris-Kay G.M., Wilkie A.O.M.;
RT "Mutations of ephrin-B1 (EFNB1), a marker of tissue boundary
RT formation, cause craniofrontonasal syndrome.";
RT Proc. Natl. Acad. Sci. U.S.A. 101:8652-8657(2004).
RN [10]
RA VARIANTS CENS ARG-27; LEU-54; SER-119; HIS-119; ALA-137; PHE-138;
RP SER-151; SER-153; TYR-153 AND ARG-182.
RX PubMed=15959873; DOI=10.1002/humu.20193;
RA Wieland I., Reardon W., Jakubiczka S., Franco B., Krese W.,
RA Vincent-Delorme C., Thierry P., Edwards M., Koenig R., Rana C.,
RA Schweiger S., Thompson E., Tinscher S., Stewart J., Wleackner P.;
RT "Twenty-six novel EFNB1 mutations in familial and sporadic
RT craniofrontonasal syndrome (CFNS).";
RT Hum. Mutat. 26:1-6(2005).
RN [11]
RA FUNCTION: Binds to the receptor tyrosine kinases EFNB1 and EFNB1.
CC binds to, and induce the collapse of, commissural axons/growth
CC cones in vitro. May play a role in conserving the orientation of
CC longitudinally projecting axons (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SUBUNIT: Interacts with GRIP1 and GRIP2.
CC -1- TISSUE SPECIFICITY: Heart, placenta, lung, liver, skeletal muscle,
CC kidney, pancreas.
CC -1- INDUCTION: By TNF-alpha.
CC -1- PTM: Inducible phosphorylation of tyrosine residues in the
CC cytoplasmic domain (By similarity).
CC -1- DISEASE: Defects in EFNB1 are a cause of craniofrontonasal

CC syndrome (CFNS) [MIM:304110]; also known as craniofrontonasal
 CC dysplasia (CFND). CFNS is an X-linked inherited syndrome
 CC characterized by hypertelorism, coronal synostosis with
 CC brachycephaly, downslanting palpebral fissures, clefting of the
 CC nasal tip, joint anomalies, longitudinally grooved fingerails and
 CC other digital anomalies.
 CC -1- SIMILARITY: Belongs to the ephrin family.
 CC
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC
 CC EMBL: U09304; AAA53093.1; -; mRNA.
 CC EMBL: U37361; AAA52369.1; -; mRNA.
 CC EMBL: U09303; AAB4127.1; -; mRNA.
 CC EMBL: AL136092; CAB86409.1; -; Genomic_DNA.
 CC EMBL: BC016649; AAH16649.1; -; mRNA.
 CC EMBL: BC052979; AAH52979.1; -; mRNA.
 CC PIR: S46993; S46993.
 CC HSSP: P52800; 1IKO.
 CC Ensembl: ENSG0000090776; Homo sapiens.
 CC HGNC: HGNC:3226; EFNBL.
 CC H-InvDB: HIX0016846; -.
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 CC Query Match 34.2%; Score 633; DB 1; Length 346;
 CC Beel Local Similarity 39.5%; Pred. No. 8.2e-33;
 CC Matches 145; Conservative 48; Mismatches 116; Indels 58; Gaps 9;
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 CC QY 8 PGGVGALLLLGLVLSGL-----SLPEVYVNSANKRFQAEQGVLPQIGRLDIL 61
 CC DB 4 PGQRWLGKLVAMVWVALCRLAPLAKNEPVSMSLNKFLSGKLVLYPKIGDLID 63
 CC QY 62 CPRAARPGRHSPNVEFYLYVGAQGRCEAPRNLLTCDRPDLRFTIKQEYS 121
 CC DB 64 CPRAEGRP-----YEVYLYVRPEQAAACSTVLDPNLVTCNREGEIRFTIKQERS 118
 CC QY 122 PVLKMGHFRSHDYIYIATSDGTRREGLESIGGVCLTRGMKYLIRVQSGPRGAVRKRV 181
 CC DB 119 PVMYGLFPRKHHDYITSTNSGLELRREGVCTRTMKIKMVGQDPNAVTPQLTT 178
 CC QY 182 SEMPMERDRGAASHLE-PGKENVPGDPTSNATSRAGELPRPMDAVGAAGLA---- 236
 CC DB 179 SRPSKRDVNTVMATAPGSRGSLGSDGKHTVNOEESGP-----GASGSSGDD 231
 CC QY 237 -----LLLLGVAAGAGA-----MCRRRRAKPSERHAPGSGSGSLGL 277
 CC DB 232 GFENSKVALFAAVGACVIFLLIIFLVLLKLRKRHKHQQ-----RAAALSL 282
 CC QY 278 ----GGGGMGPRPAGELGIALRGGAADPFCHYKVGSDYHPIYTYQDGPSP 333
 CC DB 283 STLASPKGSGTAGTEPDIILPLR---TTENNYCPHYKVGSDYGHPIYTYQDMPSP 339
 CC QY 334 PNIYKYV 340
 CC DB 340 ANIYKYV 346
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 CC RESULT 10
 CC EFNBL2 HUMAN STANDARD; PRT; 333 AA.
 CC AC P52795;
 CC DT 01-OCT-1996 (Rel. 34, Created)
 CC DT 01-OCT-1996 (Rel. 34, Last sequence update)
 CC DT 10-MAY-2005 (Rel. 47, Last annotation update)
 CC DE Ephrin-B2 precursor (EPH-related receptor tyrosine kinase ligand 5)
 CC DE (LEK-5) (HTRK-L) (HTRK-L).
 CC GN Name=EPH-B2; Synonyms=EPG5, HTRK, LEK5;
 CC OS Homo sapiens (Human).
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 CC OC Homo.

OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=96145238; PubMed=8559144; DOI=10.1016/0161-5890(95)00108-5;
 RA Cerretti D.P., Vanden Bos T., Nelson N., Kozlosky C.J., Reddy P.,
 RA Maraskovsky E., Park L.S., Lyman S.D., Copeland N.G., Gilbert D.J.,
 RA Jenkins N.A., Fletcher R.A.;
 RT "Isolation of LEK-5: a ligand of the eph-related receptor tyrosine
 RT kinases.";
 RL Mol. Immunol. 32:1197-1205(1995).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=95199254; PubMed=7534404;
 RA Bennett B.D., Zeigler F.C., Gu Q., Fendly B., Goddard A.D.,
 RA Gillett N., Matthews W.;
 RT "Molecular cloning of a ligand for the EPH-related receptor protein-
 RT tyrosine kinase Htk.";
 RL Proc. Natl. Acad. Sci. U.S.A. 92:1866-1870(1995).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=98192220; PubMed=9533549;
 RA Vogt T., Stolz W., Welsh J., Jung B., Kexbel R.S., Kobayashi H.,
 RA Landthaler M., McClelland M.;
 RT "Overexpression of Lerk-5/Bp195 messenger RNA: a novel marker for
 RT increased tumorigenicity and metastatic potential in human malignant
 RT melanomas.";
 RL Clin. Cancer Res. 4:791-797(1998).
 RN [4]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC TISSUE=Lung;
 RX MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold R.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.O., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullin S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richardson S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Buterfield V.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: Binds to the receptor tyrosine kinases EPHB4 and EPHA3.
 CC May play a role in constraining the orientation of longitudinally
 CC projecting axons (By similarity).
 CC -1- SUBUNIT: Interacts with PDZRN3 (By similarity). Binds to the
 CC receptor tyrosine kinases EPHB4 and EPHA3.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: Lung and kidney.
 CC -1- PTM: Inducible phosphorylation of tyrosine residues in the
 CC cytoplasmic domain (By similarity).
 CC -1- SIMILARITY: Belongs to the ephrin family.
 CC
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC
 CC EMBL: U16797; AAA9707.1; -; mRNA.
 CC EMBL: U38734; AAC41752.1; -; mRNA.
 CC EMBL: U81262; AAD03786.1; -; mRNA.

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DR EMBL, BC069342; AAH69342.1; -; mRNA.
DR EMBL, BC074856; AAH74856.1; -; mRNA.
DR EMBL, BC074857; AAH74857.1; -; mRNA.
DR PIR, I84743; I84743.
DR HSSP, P52800; 1IKO.
DR SMR, P52799; 27-167.
DR Ensembl; ENSG00000125266; Homo sapiens.
DR HGNC; HGNC:3227; EFN2.
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0005886; C:plasma membrane; TAS.
DR GO; GO:0046875; E:ephrin receptor binding; TAS.
DR GO; GO:0007267; P:cell-cell signaling; TAS.
DR GO; GO:000653; P:morphogenesis; TAS.
DR InterPro; IPR001799; Ephrin.
DR Pfam; PF00812; Ephrin.1.
DR PRINTS; PR01347; EPHRIN.
DR ProDom; PD002533; Ephrin.1.
DR PROSITE; PS01299; EPHRIN.1.
DR Developmental protein; Differentiation; Neurogenesis;
KM Phosphorylation; Signal; Transmembrane.
FT SIGNAL 1 27
FT CHAIN 28 333
FT TOPO_DOM 28 229
FT TRANSMEM 230 250
FT MOTIF 251 333
FT CARBOHYD 36 36
FT CARBOHYD 139 139
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FT DISULFID 89 153
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Best Local Similarity 40.9%; Pred. No. 1.1e-32;
Matches 135; Conservative 52; Mismatches 130; Indels 13; Gaps 5;

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DB 14 GVLVLCRTAISKSLVLEPIYVNSNSKFLPGQGLVLPQIGDKLDICPKV---DSKTV 70
QY 74 PNYEFKLYLVGAQGRCEAPAPNLLTCDRPDLDRFTIKFQESPNLWGHFRSH 133
DB 71 GQYEVYKVMVDKQADRCTIKKENTPLNCAKPPQDIKFTIKFQESPNLWGHFRSH 130
QY 134 DYYIATSDGTRREGSLQGVCLTRGMKVLRLVQ--SPRGAVPRKRVSEMPMER-DR 190
DB 131 DYYIISTSGSLGLELNOEGVCCOTRAMKILMKVQDASAGSTRKXDPTRRPELAGTN 190
QY 191 GAHSLPEKKNLPDPTSNATSRGAEGLPPSPMPAVAGAAGLALLLVAGAGAGMC 250
DB 191 GNSSTSPVKPNPSSSTDGNSAGHSGNNILGSEVALFAGIASGCIIFVIIITLVLL 250
QY 251 WRRRAKPSBSRHPGSGFRGSGSLGGGGGKPREAREPGLIALRGGAADPPFCFH 310
DB 251 KYRRRRHKSPQHTTLLSLTATPKRSQNN---NGSEPSDIIIPLR---TADSVFCFH 303
QY 311 YEKVSGDYGHPIYIVQDGPSPSPNIIYKV 340
DB 304 YEKVSGDYGHPIYIVQEMPPOSFANIYKV 333

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AC OSU56;
DT 10-MAY-2005 (TREMBLrel. 30, Created)
DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TREMBLrel. 30, Last annotation update)
DE Ephrin-B2 (Fragment).
GN Name=EFNB2; ORFNames=RP11-272L14.1-001;
OS Homo sapiens (human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiinae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Dunn M.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL136689; CA13907.1; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
FT NON TER 333
SQ SEQUENCE 333 AA; 36923 MW; 6D9932A632626AEA CRC64;

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Query Match 34.0%; Score 629.5; DB 2; Length 333;
Best Local Similarity 40.9%; Pred. No. 1.1e-32;
Matches 135; Conservative 52; Mismatches 130; Indels 13; Gaps 5;

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DB 14 GVLVLCRTAISKSLVLEPIYVNSNSKFLPGQGLVLPQIGDKLDICPKV---DSKTV 70
QY 74 PNYEFKLYLVGAQGRCEAPAPNLLTCDRPDLDRFTIKFQESPNLWGHFRSH 133
DB 71 GQYEVYKVMVDKQADRCTIKKENTPLNCAKPPQDIKFTIKFQESPNLWGHFRSH 130
QY 134 DYYIATSDGTRREGSLQGVCLTRGMKVLRLVQ--SPRGAVPRKRVSEMPMER-DR 190
DB 131 DYYIISTSGSLGLELNOEGVCCOTRAMKILMKVQDASAGSTRKXDPTRRPELAGTN 190
QY 191 GAHSLPEKKNLPDPTSNATSRGAEGLPPSPMPAVAGAAGLALLLVAGAGAGMC 250
DB 191 GNSSTSPVKPNPSSSTDGNSAGHSGNNILGSEVALFAGIASGCIIFVIIITLVLL 250
QY 251 WRRRAKPSBSRHPGSGFRGSGSLGGGGGKPREAREPGLIALRGGAADPPFCFH 310
DB 251 KYRRRRHKSPQHTTLLSLTATPKRSQNN---NGSEPSDIIIPLR---TADSVFCFH 303
QY 311 YEKVSGDYGHPIYIVQDGPSPSPNIIYKV 340
DB 304 YEKVSGDYGHPIYIVQEMPPOSFANIYKV 333

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AC Q9PU04;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Ephrin-B2 precursor.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Menzel P.; Pasquale E.B.;
RT "Coding sequence of chicken ephrin-B2."
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF180729; AAD53948.1; -; mRNA.
DR HSSP; P52800; 1IKO.
DR SMR; Q9PU04; 29-169.
DR Ensembl; ENSGALG0000016856; Gallus gallus.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR001799; Ephrin.
DR Pfam; PF00812; Ephrin.1.
DR PRINTS; PR01347; EPHRIN.
DR ProDom; PD002533; Ephrin.1.
DR PROSITE; PS01299; EPHRIN.1.
KM Signal.
FT SIGNAL 1 27
FT CHAIN 28 333
FT SEQUENCE 333 AA; 36761 MW; 4C28E8CB211B7783 CRC64;

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OM protein - protein search, using sw model

Run on: December 21, 2005, 14:25:04 ; Search time 27.7987 Seconds
(without alignments)
1011.187 Million cell updates/sec

Title: US-10-021-121-4

Perfect score: 1850
Sequence: 1 MGPPIHSGPGVGVGALLLG.....PVIYVDGPPQSPPIYKYV 340

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/prodata/1/aa/6/COMB.pep:*
3: /cgn2_6/prodata/1/aa/H/COMB.pep:*
4: /cgn2_6/prodata/1/aa/PCTUS/COMB.pep:*
5: /cgn2_6/prodata/1/aa/RE/COMB.pep:*
6: /cgn2_6/prodata/1/aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1850	100.0	340	2	US-08-635-130A-4	Sequence 4, Appl1
2	1850	100.0	340	2	US-09-949-016-6076	Sequence 6076, Ap
3	1850	100.0	397	2	US-09-949-016-10967	Sequence 10967, A
4	1846	99.8	340	2	US-09-214-631-3	Sequence 3, Appl1
5	1844	99.7	340	2	US-09-051-994-2	Sequence 2, Appl1
6	1841	99.5	455	2	US-08-635-130A-2	Sequence 2, Appl1
7	637.5	34.5	336	1	US-08-436-044-2	Sequence 2, Appl1
8	637.5	34.5	336	1	US-08-436-054-2	Sequence 2, Appl1
9	637.5	34.5	336	4	PCT-US95-08812-2	Sequence 2, Appl1
10	632	34.2	346	1	US-08-213-403-2	Sequence 2, Appl1
11	632	34.2	346	1	US-08-458-077-2	Sequence 2, Appl1
12	632	34.2	346	1	US-08-460-741-2	Sequence 2, Appl1
13	632	34.2	346	1	US-08-747-240-2	Sequence 2, Appl1
14	632	34.2	346	1	US-08-299-567-6	Sequence 6, Appl1
15	632	34.2	346	2	US-09-039-642B-2	Sequence 2, Appl1
16	632	34.2	346	2	US-08-635-130A-9	Sequence 9, Appl1
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18	629.5	34.0	333	1	US-08-436-044-4	Sequence 4, Appl1
19	629.5	34.0	333	1	US-08-436-054-4	Sequence 4, Appl1
20	629.5	34.0	333	2	US-08-271-948-2	Sequence 2, Appl1
21	629.5	34.0	333	2	US-08-739-333-2	Sequence 2, Appl1
22	629.5	34.0	333	2	US-09-754-105-2	Sequence 2, Appl1
23	629.5	34.0	333	2	US-09-978-339-2	Sequence 2, Appl1
24	629.5	34.0	333	2	US-08-635-130A-10	Sequence 10, Appl1
25	629.5	34.0	333	2	US-09-949-016-6453	Sequence 6453, Ap
26	629.5	34.0	333	4	PCT-US95-08534-2	Sequence 2, Appl1
27	629.5	34.0	333	4	PCT-US95-08812-4	Sequence 4, Appl1

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31	498	26.9	89	2	US-09-214-631-13	Sequence 13, Appl1
32	201	10.9	82	2	US-09-214-631-11	Sequence 11, Appl1
33	200.5	10.8	82	2	US-09-214-631-12	Sequence 12, Appl1
34	179	9.7	234	1	US-08-299-567-5	Sequence 5, Appl1
35	179	9.7	238	1	US-08-440-124-2	Sequence 2, Appl1
36	179	9.7	238	1	US-08-453-943-2	Sequence 2, Appl1
37	179	9.7	238	1	US-09-057-121-2	Sequence 2, Appl1
38	179	9.7	238	2	US-09-358-734-2	Sequence 2, Appl1
39	179	9.7	238	2	US-09-949-002-378	Sequence 378, App
40	179	9.7	238	2	US-09-949-002-413	Sequence 413, App
41	179	9.7	238	2	US-09-904-954-2	Sequence 2, Appl1
42	176.5	9.5	135	1	US-08-299-567-7	Sequence 7, Appl1
43	176	9.5	184	1	US-08-920-440B-2	Sequence 2, Appl1
44	176	9.5	184	2	US-09-173-492-2	Sequence 2, Appl1
45	176	9.5	184	2	US-09-173-133-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1
US-08-635-130A-4
; Sequence 4, Application US/08635130A

; Patent No. 6696557

; GENERAL INFORMATION:

; APPLICANT: Caras, Ingrid W

; TITLE OF INVENTION: A2-1 Neurotrophic Factor

; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:

; ADDRESSER: Genentech, Inc.

; STREET: 1 DNA Way

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WinPatIn (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/635,130A

; FILING DATE: 19-Mar-1996

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Torchia, Ph.D., Timothy E.

; REGISTRATION NUMBER: 36,700

; REFERENCE/DOCKET NUMBER: P1001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650/952-9881

; TELEFAX: 650/225-8674

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 340 amino acids

; TYPE: Amino Acid

; TOPOLOGY: linear

; US-08-635-130A-4

; Query Match

; Best Local Similarity 100.0%; Score 1850; DB 2; Length 340;

; Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MGPPIHSGPGVGVGALLLGVLGVLGSLPEPYMNSANKRFGAEGGYLYPQIGRDLU	60
DB	1	MGPPIHSGPGVGVGALLLGVLGVLGSLPEPYMNSANKRFGAEGGYLYPQIGRDLU	60
QY	61	LCPRAPPGPHSSPNTEFKLYIVGAGRCRCAPAPNILLTCDDPDDLRITTFQRY	120
DB	61	LCPRAPPGPHSSPNTEFKLYIVGAGRCRCRCAPAPNILLTCDDPDDLRITTFQRY	120

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QY 121 SPNLWGHEFRSHHDYIIATSDGTGEGESLGGVCLTGMKYLTVGSGPGGAVERKP 180
Db 121 SPNLWGHEFRSHHDYIIATSDGTGEGESLGGVCLTGMKYLTVGSGPGGAVERKP 180
QY 181 VSEMERDRGAASHLEPEKENLPQDPTSNATSRGAEGPLPPSPMAVGAAGGLALLL 240
Db 181 VSEMERDRGAASHLEPEKENLPQDPTSNATSRGAEGPLPPSPMAVGAAGGLALLL 240
QY 241 GVAGAGGAMCWRRRRAKPSSESHHPGSGSGRGSLGLGGGGMGPREAPGELGIALRG 300
Db 241 GVAGAGGAMCWRRRRAKPSSESHHPGSGSGRGSLGLGGGGMGPREAPGELGIALRG 300
QY 301 GAADPPFCBHYEKVSGDYGHPYIIVODGPPQSPNNIYKV 340
Db 301 GAADPPFCBHYEKVSGDYGHPYIIVODGPPQSPNNIYKV 340

RESULT 2
US-09-949-016-6076
; Sequence 6076, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6076
; LENGTH: 340
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-6076

Query Match 100.0%; Score 1850; DB 2; Length 340;
Best Local Similarity 100.0%; Pred. No. 1.1e-148;
Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGPPSHSGGVAVGALLLGLVGLVSGLSLEPYVMNSANKRFOAEGGYLYLPDGRDL 60
Db 1 MGPPSHSGGVAVGALLLGLVGLVSGLSLEPYVMNSANKRFOAEGGYLYLPDGRDL 60
QY 61 LCPRARPPGPHSSPNVEFYKLYLVGAQGRCEAPAPNLLTCDRPDLDLRTIKFOEY 120
Db 61 LCPRARPPGPHSSPNVEFYKLYLVGAQGRCEAPAPNLLTCDRPDLDLRTIKFOEY 120
QY 121 SPNLWGHEFRSHHDYIIATSDGTGEGESLGGVCLTGMKYLTVGSGPRGAVPRKP 180
Db 121 SPNLWGHEFRSHHDYIIATSDGTGEGESLGGVCLTGMKYLTVGSGPRGAVPRKP 180
QY 181 VSEMERDRGAASHLEPEKENLPQDPTSNATSRGAEGPLPPSPMAVGAAGGLALLL 240
Db 181 VSEMERDRGAASHLEPEKENLPQDPTSNATSRGAEGPLPPSPMAVGAAGGLALLL 240
QY 241 GVAGAGGAMCWRRRRAKPSSESHHPGSGSGRGSLGLGGGGMGPREAPGELGIALRG 300
Db 241 GVAGAGGAMCWRRRRAKPSSESHHPGSGSGRGSLGLGGGGMGPREAPGELGIALRG 300
QY 301 GAADPPFCBHYEKVSGDYGHPYIIVODGPPQSPNNIYKV 340
Db 301 GAADPPFCBHYEKVSGDYGHPYIIVODGPPQSPNNIYKV 340

RESULT 3
US-09-949-016-10967

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Sequence 10967, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C0001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10967
LENGTH: 397
TYPE: PRT
ORGANISM: Human
US-09-949-016-10967

Query Match      100.0%; Score 1850; DB 2; Length 397;
Best Local Similarity 100.0%; Pred. No. 1,3e-148;
Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  MGPHSGPGQVRVGAALLLVGLVGLVGLSLSEBPVYNSANKRFOAEGGYLVYPQIGDRLDL 60
DB      58  MGPHSGPGQVRVGAALLLVGLVGLVGLSLSEBPVYNSANKRFOAEGGYLVYPQIGDRLDL 117

QY      61  LCPRAAPRPGHSSRNVEFFYKLYVAGACGRCEAAPAPLLTTCRPRDLAFTTFQXY 120
DB      118  LCPRAAPRPGHSSRNVEFFYKLYVAGACGRCEAAPAPLLTTCRPRDLAFTTFQXY 177

QY      121  SPNLMGHEFRHNDHYIYIATSDGTREGESLQGGVCLTRGMKYLRLVGQSPRGAVPRKP 180
DB      178  SPNLMGHEFRHNDHYIYIATSDGTREGESLQGGVCLTRGMKYLRLVGQSPRGAVPRKP 237

QY      181  VSEMPMERDRCAHSLSEBKENTLPDPTSNATSRGAEGLPPSPMPAVAGAGGALLLL 240
DB      238  VSEMPMERDRCAHSLSEBKENTLPDPTSNATSRGAEGLPPSPMPAVAGAGGALLLL 297

QY      241  GVAGAGGAMCRRRRKAKSESRRHQPQSGFGRGSGLGLGGGGMGREAPRGLGILNRG 300
DB      298  GVAGAGGAMCRRRRKAKSESRRHQPQSGFGRGSGLGLGGGGMGREAPRGLGILNRG 357

QY      301  GAADPPFCPHYEKVSGDYGHFVYIYQDGPQSPPIIYKYV 340
DB      358  GAADPPFCPHYEKVSGDYGHFVYIYQDGPQSPPIIYKYV 397

RESULT 4
US-09-214-631-3
; Sequence 3, Application US/09214631
; Patent No. 6413730
; GENERAL INFORMATION:
; APPLICANT: Holland, Sacha
; APPLICANT: Mbamalu, Geraldine
; APPLICANT: Rawson, Tony
; TITLE OF INVENTION: OLIGOMERIZED RECEPTORS WHICH AFFECT PATHWAYS REGULATED
; TITLE OF INVENTION: BY TRANSMEMBRANE LIGANDS FOR ELK-RELATED RECEPTOR
; FILE REFERENCE: 11757.23USWO
; CURRENT APPLICATION NUMBER: US/09/214,631
; CURRENT FILING DATE: 1999-03-12
; EARLIER APPLICATION NUMBER: PCT/CA97/00473
; EARLIER FILING DATE: 1997-07-04
; EARLIER APPLICATION NUMBER: 60/021,272
; EARLIER FILING DATE: 1996-07-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3

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LENGTH: 340
TYPE: PRT
ORGANISM: Homo sapiens
US-09-214-631-3

Query Match 99.8%; Score 1846; DB 2; Length 340;
Best Local Similarity 99.7%; Pred. No. 2, 4e-148;
Matches 339; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 MGPBHSFGVGVGALLLGLVGLVSGLSLEPYWNSANKRFOAEGGYLYLPQIGRLDL 60
1 MGPBHSFGVGVGALLLGLVGLVSGLSLEPYWNSANKRFOAEGGYLYLPQIGRLDL 60
61 LCPBAPPPGHSPPNTEFYKLYLVGAQGRCAAPAPNLLTCDPBDLRTTIKFOEY 120
61 LCPBAPPPGHSPPNTEFYKLYLVGAQGRCAAPAPNLLTCDPBDLRTTIKFOEY 120
121 SPULWHEFRSHHDYIITS DGTREGLSLQGVCLTRGMKVLRVGSPRGAVPRKP 180
121 SPULWHEFRSHHDYIITS DGTREGLSLQGVCLTRGMKVLRVGSPRGAVPRKP 180
181 VSEMPERDRGAHSLPEKENVPGDPTSNATSRGAEGPLPPSPMAVGAAGLALLL 240
181 VSEMPERDRGAHSLPEKENVPGDPTSNATSRGAEGPLPPSPMAVGAAGLALLL 240
241 GVAAGAGAMCWRRRRRAKPSRHPGSGFGRGSLGLGGGGMGPPEABPGLIALRG 300
241 GVAAGAGAMCWRRRRRAKPSRHPGSGFGRGSLGLGGGGMGPPEABPGLIALRG 300
301 GAADPFCEHYEKVSGDYGHPYIYVODGPQSPNITYKV 340
301 GAADPFCEHYEKVSGDYGHPYIYVODGPQSPNITYKV 340

RESULT 5
US-09-051-994-2
Sequence 2, Application US/09051994A
Patent No. 6602683
GENERAL INFORMATION:
APPLICANT: REGENERON PHARMACEUTICALS, INC.
TITLE OF INVENTION: BIOLOGICALLY ACTIVE EPH FAMILY LIGANDS
FILE REFERENCE: REG-341-PCT-US
CURRENT APPLICATION NUMBER: US/09/051, 994A
CURRENT FILING DATE: 1998-04-24
EARLIER APPLICATION NUMBER: PCT/US96/17201
EARLIER FILING DATE: 1996-10-25
EARLIER APPLICATION NUMBER: 60/007, 015
EARLIER FILING DATE: 1995-10-25
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 2
LENGTH: 340
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: site
LOCATION: (166)
OTHER INFORMATION: Xaa=Arg or Glu
US-09-051-994-2

Query Match 99.7%; Score 1844; DB 2; Length 340;
Best Local Similarity 99.7%; Pred. No. 3, 5e-148;
Matches 339; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

121 SPULWHEFRSHHDYIITS DGTREGLSLQGVCLTRGMKVLRVGSPRGAVPRKP 180
181 VSEMPERDRGAHSLPEKENVPGDPTSNATSRGAEGPLPPSPMAVGAAGLALLL 240
181 VSEMPERDRGAHSLPEKENVPGDPTSNATSRGAEGPLPPSPMAVGAAGLALLL 240
241 GVAAGAGAMCWRRRRRAKPSRHPGSGFGRGSLGLGGGGMGPPEABPGLIALRG 300
241 GVAAGAGAMCWRRRRRAKPSRHPGSGFGRGSLGLGGGGMGPPEABPGLIALRG 300
301 GAADPFCEHYEKVSGDYGHPYIYVODGPQSPNITYKV 340
301 GAADPFCEHYEKVSGDYGHPYIYVODGPQSPNITYKV 340

RESULT 6
US-08-635-130A-2
Sequence 2, Application US/08635130A
Patent No. 6696557
GENERAL INFORMATION:
APPLICANT: Caras, Ingrid W
TITLE OF INVENTION: A2-1 Neurotrophic Factor
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/635, 130A
FILING DATE: 19-Mar-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Phd., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 455 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-635-130A-2

Query Match 99.5%; Score 1841; DB 2; Length 455;
Best Local Similarity 100.0%; Pred. No. 9e-148;
Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	Db	QY	Db
241	GVAGAGGACMCRRRRRAKPEESHPGGSFGRSGSLGLGGGGGMPREAPPEGLIALRG 3 0 0	301	GAADPPFCPHYENSGDGHFVYIYVDGSPQSPFPIIYY 3 3 8
241	GVAGAGGACMCRRRRRAKPEESHPGGSFGRSGSLGLGGGGGMPREAPPEGLIALRG 3 0 0	301	GAADPPFCPHYENSGDGHFVYIYVDGSPQSPFPIIYY 3 3 8

RESULT 7
US-08-436-044-2

Query Match 34.5%; Score 637.5; DB 1; length 336;

QY	251	MRPRRAKPSBESHPGSGRGSGSLGLGGGGGMCGRBRAEPGLGALRGGGAADPPRC	310
Db	254	KYRRRRKRKISPGHTTTLSTLTATKRCGN-----NGSEPVDVILPR--TADSVCPH	306
QY	311	YERKSGDYGHFVYTYQDGPQSPSPNIIYKYV	340
Db	307	YERKSGDYGHFVYIVDEMPQSPFNIIYKYV	336

RESULT 8
US-08-436-054-2

Query Match	34.5%	Score 637.5	DB 1	Length 336
Best Local Similarity	42.1%	Pred. No. 4.9e-46		
Matches 139	Conservative 49	Mismatches 129	Indels 13	Gaps 5

Db 194 GRSSITSPVKPNPGSSTDGNSAGHSGNNLGSEVALFAGIASGCIIFIVIIITLVLL 253

Db 254 KVRRRRRKSPQHTTLLSLTLATPRKGN-----NGSEPSDVIPLR---TADSVFCH 306
QY 311 YEKVSGDYGHPPYIVODGPPSPNNIYKYV 340
Db 307 YEKVSGDYGHPPYIVQEMPPSPANNIYKYV 336

RESULT 9

PCT-US95-08812-2
; Sequence 2, Application PC/TUS9508812
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; TITLE OF INVENTION: HTK LIGAND
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Path (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/08812
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: 902PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELE: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 336 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; PCT-US95-08812-2

Query Match 34.5%; Score 637.5; DB 4; Length 336;

Best Local Similarity 42.1%; Pred. No. 4,9e-46; Matches 139; Conservative 49; Mismatches 129; Indels 13; Gaps 5;

QY 14 GALLLGLVGLVSGLEPEVYNNANKRFQAEQGVYVYQIGDRDLDCPPRAPPPHSS 73
Db 17 GLLMVLCRAIRSRISYLEPIYNNSSSKRLPGGLVLPQIGDKDILCPYV---DSKTV 73
QY 74 PNYEFKYLTVGAGRCRCEAPAPNLLITCDRDLRLFTIKFOEYSNLMGHEFRSH 133
Db 74 GQVEYKVMVMDKQDRCTIKENTPLINCARDPDQVFTIKFOEYSNLMGHEFRSH 133
QY 134 DVIYIATSGTREGLESLOGGVCLTGMKVLARVQ--SPRGAVPRKVSSEMPER-DR 190
Db 134 DVIYIISTSGSLGLELNOEGVCQTAMKILMKVGDASASARNHGTRRPELSAGTN 193
QY 191 GAHSLPEKENVLPDPTSNATSRGAEGLPPSPMPAVAGLAAGLALLLLGVAAGAMC 250
Db 194 GSSSTTSPVKNPSSSTGNSAGSHGNNLLGSEVALPAGIASGCIIFVIIITVVLL 253
QY 251 WRRRAKPSSESHPPGSGFGRGSLGLGGGGMGPPEALPEGLALRGGAADPPFCH 310
Db 254 KVRRRRRKSPQHTTLLSLTLATPRKGN-----NGSEPSDVIPLR---TADSVFCH 306

QY 311 YEKVSGDYGHPPYIVODGPPSPNNIYKYV 340
Db 307 YEKVSGDYGHPPYIVQEMPPSPANNIYKYV 336

RESULT 10

US-08-213-403-2
; Sequence 2, Application US/08213403
; Patent No. 5512457
; GENERAL INFORMATION:
; APPLICANT: Lyman, Stewart D.
; APPLICANT: Beckmann, M. Patricia
; APPLICANT: Baum, Peter R.
; APPLICANT: Carpenter, Melissa
; TITLE OF INVENTION: No. 5512457el Cytokine Designated elk ligand
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple System 7.1
; SOFTWARE: Microsoft Word for Apple, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/213,403
; FILING DATE: 15-MAR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,693
; FILING DATE: 13-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2807-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 346 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-213-403-2

Query Match 34.2%; Score 632; DB 1; Length 346;

Best Local Similarity 39.5%; Pred. No. 1.5e-45; Matches 145; Conservative 48; Mismatches 116; Indels 58; Gaps 9;

QY 8 PGVYVGLALLGLVGLVSGLEPEVYNNANKRFQAEQGVYVYQIGDRDLDCPPRAPPPHSS 61
Db 4 PGQRLGKVLVAMVVMALCRLATPLAKNLEFVSSNLPKFTSGGLVLYTPQIGDKDII 63
QY 62 CPRAPPPHSSPNYEFKYLTVGAGRCRCEAPAPNLLITCDRDLRLFTIKFOEYS 121
Db 64 CPRAEAGR-----YEVYLVYVRPEQAACSTVLDPNVLVTCNRPQGIKFOEYS 118
QY 122 PNLNHERSHNDYIYIATSDGTREGLESLOGGVCLTGMKVLARVQ--SPRGAVPRKVS 161
Db 119 PNYMGLFEKQHDYIYIATSDGTREGLESLOGGVCLTGMKVLARVQ--SPRGAVPRKVS 178
QY 182 SEMPERDRGAHSLPEKENVLPDPTSNATSRGAEGLPPSPMPAVAGLAAGLALLLLGVAAGAMC 236
Db 179 SRPSKADNTVYMAAQAGSRGSLDSDGKHETTVNQEKSGL-----GASGSSGDPD 231
QY 237 -----LALLGVAAGLA-----MWRRRRAKPSSESHPPGSGFGRGSLGL 277
Db 232 GFNSKVALFAVAGCVIFLLIITFLVTLVLLKLRKRKHQO-----RAAALSL 282

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QY 278 ----GGGGMGPBREPGLGIALRGGAADPPFCPHYEKVSGDYGHPIYIVODGPPQSP 333
DB 283 STLSPKSGSGTAGTPEPDIITPLR---TTENNYPHYEKVSGDYGHPIYIVQEMPPQSP 339
QY 334 PNYYKV 340
DB 340 ANYYKV 346

RESULT 11
US-08-458-077-2
; Sequence 2, Application US/08458077
; Patent No. 5627267
; GENERAL INFORMATION:
; APPLICANT: Lyman, Stewart D.
; APPLICANT: Beckmann, M. Patricia
; APPLICANT: Baum, Peter R.
; APPLICANT: Carpenter, Melissa
; TITLE OF INVENTION: No. 5627267el Cytokine Designated elk Ligand
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple System 7.1
; SOFTWARE: Microsoft Word for Apple, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,077
; FILING DATE: 01-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/213,403
; FILING DATE: 15-MAR-1994
; APPLICATION NUMBER: US 07/977,693
; FILING DATE: 13-NOV-1992
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2807-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 346 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-458-077-2

Query Match 34.2%; Score 632; DB 1; Length 346;
Best Local Similarity 39.5%; Pred. No. 1.5e-45;
Matches 145; Conservative 48; Mismatches 116; Indels 50; Gaps 9;

QY 8 PGGVVGLLLGLVGLVSGL-----SLEPYWNSANKRFOAEGGYLYVPOIGRLDIL 61
DB 4 PGQRWLGGKLVAMVWALCRLATPLAKNLEPVSWSLNPKFLSGKGLVYTPKIGDKLDIT 63
QY 62 CPBAPPGGHSPPNTEFYLYIVGGAQGRCAAPPANILLTCRPPDLRLFTIKFOEYS 121
DB 64 CPBAPPGGHSPPNTEFYLYIVGGAQGRCAAPPANILLTCRPPDLRLFTIKFOEYS 118
QY 122 PVLKHEHPSHHDYITATSDGTREGESLGGVCLTRGMKVLVVGOSPRGGAVPKRV 181
DB 119 PNYMGLERKQHDHYITSTNSGLBGLENREGGVCKTRIMKIMKVGODPNAVTPBOLTT 178
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QY 182 SEMPERDRGAHSLLE-PEKENTLPGDPTSNATSRGAEGLPAPPMPAVAGAAGLA---- 236
DB 179 SRPSKADUNVTYMATQVARSRLSDSDKHEVTVAQEKSGP-----GAGSGSSGDDP 231
QY 237 -----LILLVAGAGGA-----MCFRRRAKPSBSRHPGSGTGRGSLGL 277
DB 232 GFENSKVALFAAVGACVIFLLIIFLVLLKRRKRKHQO-----RAAALSL 282
QY 278 ----GGGGMGPBREPGLGIALRGGAADPPFCPHYEKVSGDYGHPIYIVODGPPQSP 333
DB 283 STLSPKSGSGTAGTPEPDIITPLR---TTENNYPHYEKVSGDYGHPIYIVQEMPPQSP 339
QY 334 PNYYKV 340
DB 340 ANYYKV 346

RESULT 12
US-08-460-741-2
; Sequence 2, Application US/08460741
; Patent No. 5670625
; GENERAL INFORMATION:
; APPLICANT: Lyman, Stewart D.
; APPLICANT: Beckmann, M. Patricia
; APPLICANT: Baum, Peter R.
; APPLICANT: Carpenter, Melissa
; TITLE OF INVENTION: No. 5670625el Cytokine Designated elk Ligand
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple System 7.1
; SOFTWARE: Microsoft Word for Apple, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,741
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/213,403
; FILING DATE: 15-MAR-1994
; APPLICATION NUMBER: US 07/977,693
; FILING DATE: 13-NOV-1992
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2807-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 346 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-460-741-2

Query Match 34.2%; Score 632; DB 1; Length 346;
Best Local Similarity 39.5%; Pred. No. 1.5e-45;
Matches 145; Conservative 48; Mismatches 116; Indels 50; Gaps 9;

QY 8 PGGVVGLLLGLVGLVSGL-----SLEPYWNSANKRFOAEGGYLYVPOIGRLDIL 61
DB 4 PGQRWLGGKLVAMVWALCRLATPLAKNLEPVSWSLNPKFLSGKGLVYTPKIGDKLDIT 63
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[illegible]

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RESULT 13
US-08-747-240-2
; Sequence 2, Application US/08747240
; Patent No. 5728813
; GENERAL INFORMATION:
; APPLICANT: Lyman, Stewart D.
; APPLICANT: Beckmann, M. Patricia
; APPLICANT: Baum, Peter R.
; APPLICANT: Carpenter, Melissa
; TITLE OR INVENTION: No. 5728813el Cytokine Designated elc Ligand
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple System 7.1
; SOFTWARE: Microsoft Word for Apple, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/747,240
; FILING DATE: 12-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/213,403
; FILING DATE: 15-MAR-1994
; APPLICATION NUMBER: US 07/977,693
; FILING DATE: 13-NOV-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Seege, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2807-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 346 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULAR TYPE: protein
; US-08-747-240-2

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Query Match	34.2%;	Score 632;	DB 1;	Length 346;
Best Local Similarity	39.5%;	Pred. No. 1.5e-45;		
Matches 145;	Conservative 48;	Mismatches 116;	Indels 58;	Gaps 9;

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QY      62 CPRARPFGHSSPNTEFYKLYLVGSAQGRCEBAPRNLLITCDRPLDLRFITTKFOEYS 121
Db      64 CPRAEAGRP-----YEYKLYLVPRBEOAAACSTVLDPVLTVCNRPQOEIRFTIKFOEFS 118

QY      122 PNLMGHEPSSHHDYITIAITDOSTRGESLQGVYCLTRGMKVLLLRVQSPRGCAVPRKPV 181
Db      119 PNTMGLEFPKHHDYITSTNSGSLGLENNRGSCFRTRMKYLKVKVQDPNAVTPBOLTT 178

QY      182 SEYPMERDRGAHSLE-PKENLPDPDPSNATSGAEGPLRPPEMAPVAGAAGLA----- 236
Db      179 SRPSKADNTVCKAIOAQPSRSGSLGSDSGKHETYNQOEKSP-----GASGSSSGDPD 231

QY      237 -----LLLLVAGAGCA-----MCMRRRRAPKSESRRHPGSGFGRGSLGL 277
Db      232 GFENSKVALFAAVGAGCVIFLLIITFLTVLLIKLRKRRHKITQ-----RAALSL 282

QY      278 -----GGGGGNGRERABPGEIGIALRGGAADPPFCPHYERKYSGLYGHYVITYDDGPPQSP 333
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QY      334 PNITYYKV 340
Db      340 ANITYYKV 346

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1      RESULT 14.
2      US-08-299-567-6
3      Sequence 6: Application US/08299567
4      Patent No. 5747033
5      GENERAL INFORMATION:
6      APPLICANT: Davis, et al.
7      TITLE OF INVENTION: METHOD OF ENHANCING THE BIOLOGICAL
8      TITLE OF INVENTION: ACTIVITY OF BPH FAMILY LIGANDS
9      NUMBER OF SEQUENCES: 8
10     CORRESPONDENCE ADDRESS:
11     ADDRESSEE: Regeneron Pharmaceuticals, Inc.
12     STREET: 777 Old Saw Mill River Road
13     CITY: Tarrytown
14     STATE: New York
15     COUNTRY: U.S.A.
16     ZIP: 10591-6707
17     COMPUTER READABLE FORM:
18     MEDIUM TYPE: Floppy disk
19     COMPUTER: IBM PC compatible
20     OPERATING SYSTEM: PC-DOS/MS-DOS
21     SOFTWARE: Patentin Release
22     CURRENT APPLICATION DATA:
23     APPLICATION NUMBER: US/08/299,567
24     FILING DATE: 01-SEP-1994
25     CLASSIFICATION: 435
26     ATTORNEY/AGENT INFORMATION:
27     NAME: Kempster, Gail M.
28     REGISTRATION NUMBER: 32,143
29     REFERENCE/DOCKET NUMBER: REG 290
30     TELECOMMUNICATION INFORMATION:
31     TELEPHONE: 914-345-7400
32     TELEFAX: 914-345-7721
33     INFORMATION FOR SEQ ID NO: 6:
34     SEQUENCE CHARACTERISTICS:
35     LENGTH: 346 amino acids
36     TYPE: amino acid
37     STRANDEDNESS:
38     TOPOLOGY: unknown
39     MOLECULE TYPE: protein

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US-08-299-567-6

Query Match 34.2%; Score 632; DB 1; Length 346;
Best Local Similarity 39.5%; Pred. No. 1.5e-45;
Matches 145; Conservative 48; Mismatches 116; Indels 58; Gaps 9;

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OY 8 PGGVVGVALLLLGLVLSGL-----SLEPVYVNSANKRFOAEGGYLYPOIGRLDIL 61
DB 4 PGQRMIGKVLVMMVWVALCRLATPLAKNLEPVSWSLNPKFLSGKGLVYIPKIGDLDIT 63
OY 62 CRRARPGHSSBNFYCLYLVGAGQGRCEAPRNILLTCDRDLRLRTIKFOEYS 121
DB 64 CRRARPGHSSBNFYCLYLVGAGQGRCEAPRNILLTCDRDLRLRTIKFOEYS 118
OY 122 PVLWGHFRSHHDYIATSDGTREGLESLOGVCLTRGKMLLRVYGOSPRGGAVPRKPV 181
DB 119 PNYMGLFKKHHDIYITTSNSGSLGLENNREGVCTRIMKIIIMKVGODPNVATPEQLTT 178
OY 182 SEMPMERDRGAHSLP-PGKENTLPGDPTSNATSRGAEGPLPPSPMVAAGAAGLA---- 236
DB 179 SRPSKEADNTVMMATQAPGSRGSLGDSGKHETVNOEKGSP-----GASGSSGDPD 231
OY 237 -----LILLVAGAGGA-----MCRRRRAKPSBSRHPGSGFRGSGSLGL 277
DB 232 GFENSKVALFAAVGACVIFLLIIIFLVLLLKLRKRHRKHTQO-----RAAALS 282
OY 278 -----GGGGMGPREAPGELGIALRGGAADPPFCPHYEKVSGDYGHPIYIVODGPPOSP 333
DB 283 STLAPKXGSGTAGTSPDIIIPLR---TTENNYPCHYEKVSQDYGHPYIVQENPPOSP 339
OY 334 PNIYYKV 340
DB 340 ANIYYKV 346
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RESULT 15

US-09-039-642B-2

; Sequence 2, Application US/09039642B
; Patent No. 6540992
; GENERAL INFORMATION:
; APPLICANT: Lyman, Stewart D.
; APPLICANT: Beckmann, W. Patricia
; APPLICANT: Baum, Peter R.
; APPLICANT: Carpenter, Melissa K.
; TITLE OF INVENTION: NOVEL CYTOKINE DESIGNATED ELK LIGAND
; FILE REFERENCE: GENENT 67CPDV3
; CURRENT APPLICATION NUMBER: US/09/039,642B
; CURRENT FILING DATE: 1998-03-16
; PRIOR APPLICATION NUMBER: 08/213,403
; PRIOR FILING DATE: 1994-03-15
; PRIOR APPLICATION NUMBER: 07/977,693
; PRIOR FILING DATE: 1992-11-13
; PRIOR APPLICATION NUMBER: 08/747,240
; PRIOR FILING DATE: 1996-10-12
; PRIOR APPLICATION NUMBER: 08/460,741
; PRIOR FILING DATE: 1995-06-02
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FaastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-039-642B-2

Query Match 34.2%; Score 632; DB 2; Length 346;
Best Local Similarity 39.5%; Pred. No. 1.5e-45;
Matches 145; Conservative 48; Mismatches 116; Indels 58; Gaps 9;

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OY 8 PGGVVGVALLLLGLVLSGL-----SLEPVYVNSANKRFOAEGGYLYPOIGRLDIL 61
DB 4 PGQRMIGKVLVMMVWVALCRLATPLAKNLEPVSWSLNPKFLSGKGLVYIPKIGDLDIT 63
OY 62 CRRARPGHSSBNFYCLYLVGAGQGRCEAPRNILLTCDRDLRLRTIKFOEYS 121
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DB 64 CRRARPGHSSBNFYCLYLVGAGQGRCEAPRNILLTCDRDLRLRTIKFOEYS 118
OY 122 PVLWGHFRSHHDYIATSDGTREGLESLOGVCLTRGKMLLRVYGOSPRGGAVPRKPV 181
DB 119 PNYMGLFKKHHDIYITTSNSGSLGLENNREGVCTRIMKIIIMKVGODPNVATPEQLTT 178
OY 182 SEMPMERDRGAHSLP-PGKENTLPGDPTSNATSRGAEGPLPPSPMVAAGAAGLA---- 236
DB 179 SRPSKEADNTVMMATQAPGSRGSLGDSGKHETVNOEKGSP-----GASGSSGDPD 231
OY 237 -----LILLVAGAGGA-----MCRRRRAKPSBSRHPGSGFRGSGSLGL 277
DB 232 GFENSKVALFAAVGACVIFLLIIIFLVLLLKLRKRHRKHTQO-----RAAALS 282
OY 278 -----GGGGMGPREAPGELGIALRGGAADPPFCPHYEKVSGDYGHPIYIVODGPPOSP 333
DB 283 STLAPKXGSGTAGTSPDIIIPLR---TTENNYPCHYEKVSQDYGHPYIVQENPPOSP 339
OY 334 PNIYYKV 340
DB 340 ANIYYKV 346
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Search completed: December 21, 2005, 14:37:39
Job time : 28.7987 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: December 21, 2005, 14:30:39 ; Search time 95.7987 Seconds
(without alignments)
1482.921 Million cell updates/sec

Title: US-10-021-121-4

Perfect score: 1850
Sequence: 1 MGPPIHSGPGVIRGALLILG.....PYIVQDPSPSPNIVYK 340

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:
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2: /cgn2_6/prodata/1/pubppa/US08_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1850	100.0	340	4	US-10-021-121-4 Sequence 4, Appl1
2	1850	100.0	340	5	US-10-723-860-4256 Sequence 4256, Ap
3	1850	100.0	340	5	US-10-698-907-16 Sequence 16, Appl1
4	1846	99.8	340	4	US-10-138-787-3 Sequence 3, Appl1
5	1844	99.7	340	4	US-10-417-924A-2 Sequence 2, Appl1
6	1841	99.5	455	4	US-10-021-121-2 Sequence 2, Appl1
7	1780	96.2	340	5	US-10-698-907-8 Sequence 8, Appl1
8	1559	84.3	285	4	US-10-408-765A-2695 Sequence 2695, Ap
9	637.5	34.5	336	5	US-10-698-907-7 Sequence 9, Appl1
10	632	34.2	346	4	US-10-021-121-10 Sequence 2, Appl1
11	632	34.2	346	4	US-10-356-289-2 Sequence 2, Appl1
12	632	34.2	346	4	US-10-712-124-60 Sequence 60, Appl1
13	632	34.2	346	5	US-10-789-378-30 Sequence 30, Appl1
14	632	34.2	346	5	US-10-698-907-14 Sequence 14, Appl1
15	629.5	34.0	333	3	US-09-754-105-2 Sequence 2, Appl1
16	629.5	34.0	333	3	US-09-878-339-2 Sequence 2, Appl1
17	629.5	34.0	333	4	US-10-021-121-10 Sequence 10, Appl1
18	629.5	34.0	333	4	US-10-311-496A-63 Sequence 63, Appl1
19	629.5	34.0	333	5	US-10-696-639-62 Sequence 62, Appl1
20	629.5	34.0	333	5	US-10-698-907-15 Sequence 15, Appl1
21	629.5	34.0	333	5	US-10-800-350-396 Sequence 396, App
22	629.5	34.0	333	5	US-10-800-077-396 Sequence 396, App
23	622.5	33.6	333	4	US-10-138-787-4 Sequence 4, Appl1
24	613.5	33.2	345	5	US-10-698-907-6 Sequence 6, Appl1
25	608.5	32.9	345	5	US-10-138-787-5 Sequence 5, Appl1
26	498	26.9	89	3	US-09-862-179A-17 Sequence 17, Appl1
27	498	26.9	89	4	US-10-138-787-13 Sequence 13, Appl1

28	447	24.2	229	5	US-10-698-907-20	Sequence 20, Appl1
29	446.5	24.1	459	5	US-10-800-350-390	Sequence 390, App
30	446.5	24.1	459	5	US-10-800-077-390	Sequence 390, App
31	443	23.9	226	5	US-10-698-907-21	Sequence 21, Appl1
32	442	23.9	233	5	US-10-800-350-388	Sequence 388, Appl1
33	442	23.9	233	5	US-10-800-077-388	Sequence 388, App
34	284.5	15.4	92	3	US-09-864-761-48262	Sequence 48262, A
35	205.5	11.1	136	3	US-09-864-761-48257	Sequence 48257, A
36	202.5	10.9	106	3	US-09-925-297-639	Sequence 639, App
37	201	10.9	82	3	US-09-862-179A-15	Sequence 15, Appl1
38	201	10.9	82	4	US-10-138-787-11	Sequence 11, Appl1
39	200.5	10.8	82	3	US-09-862-179A-16	Sequence 16, Appl1
40	200.5	10.8	82	4	US-10-138-787-12	Sequence 12, Appl1
41	182	9.8	652	6	US-11-097-143-2655	Sequence 2655, App
42	182	9.8	652	6	US-11-097-143-2655	Sequence 23436, A
43	179	9.7	238	3	US-09-904-954-2	Sequence 2, Appl1
44	179	9.7	238	3	US-09-733-756-2	Sequence 2, Appl1
45	179	9.7	238	4	US-10-241-220-72	Sequence 72, Appl1

ALIGNMENTS

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RESULT 1
US-10-021-121-4
; Sequence 4, Application US/10021121
; Publication No. US2002014244A1
;
GENERAL INFORMATION:
;
APPLICANT: Caras, Ingrid M
;
TITLE OF INVENTION: A2-1 Neurotrophic Factor
;
NUMBER OF SEQUENCES: 10
;
CORRESPONDENCE ADDRESSES:
;
ADDRESSEE: Genentech, Inc.
;
STREET: 1 DNA Way
;
CITY: South San Francisco
;
STATE: California
;
COUNTRY: USA
;
ZIP: 94080
;
COMPUTER READABLE FORM:
;
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;
COMPUTER: IBM PC compatible
;
OPERATING SYSTEM: PC-DOS/MS-DOS
;
SOFTWARE: WinPatlin (Genentech)
;
CURRENT APPLICATION DATA:
;
APPLICATION NUMBER: US/10/021,121
;
FILING DATE: 06-Dec-2001
;
CLASSIFICATION: <Unknown>
;
PRIOR APPLICATION DATA:
;
APPLICATION NUMBER: US/08/635,130
;
FILING DATE: 19-Mar-1996
;
ATTORNEY/AGENT INFORMATION:
;
NAME: Torchia, PhD., Timothy E.
;
REGISTRATION NUMBER: 36,700
;
REFERENCE/DOCKET NUMBER: P1001
;
TELECOMMUNICATION INFORMATION:
;
TELEPHONE: 650/225-8674
;
TELEFAX: 650/952-9881
;
INFORMATION FOR SEQ ID NO: 4:
;
SEQUENCE CHARACTERISTICS:
;
LENGTH: 340 amino acids
;
TYPE: Amino Acid
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TOPOLOGY: Linear
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SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-021-121-4
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Query Match 100.0%; Score 1850; DB 4; Length 340;
Best Local Similarity 100.0%; Pred. No. 3.5e-131;
Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGPPIHSGPGVIRGALLILGVLGVSLPEPYNNANKRFOAEGGYLYPIQIGRLDL 60
DB 1 MGPPIHSGPGVIRGALLILGVLGVSLPEPYNNANKRFOAEGGYLYPIQIGRLDL 60

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DB 121 SPNLWHERSHHDYIITATSDGTREGLESLOGGVCLTRGMKVLRLVGOSPRGGAVERP 180
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QY 301 GAADPPFCPHYEKVSGDYGHPIYIVODGPPOSPPNIYKYV 340
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DB 301 GAADPPFCPHYEKVSGDYGHPIYIVODGPPOSPPNIYKYV 340
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RESULT 2

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US-10-723-860-4256
/ Sequence 4256, Application US/10723860
/ Publication No. US2004023606A1
/ GENERAL INFORMATION:
/ APPLICANT: Aziz, Nacasha
/ APPLICANT: Gineburg, Wendy M.
/ TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
/ FILE REFERENCE: 05882.0193.NPDS01
/ CURRENT APPLICATION NUMBER: US/10/723,860
/ PRIOR FILING DATE: 2003-11-26
/ PRIOR APPLICATION NUMBER: 60/429,739
/ NUMBER OF SEQ ID NOS: 8393
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 4256
/ LENGTH: 340
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-723-860-4256
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Query Match 100.0%; Score 1850; DB 5; Length 340;
Best Local Similarity 100.0%; Pred. No. 3.5e-131;
Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MGPPHSGPGGVVVGALLLGLVGLVSGLSLEPVYVNSANKRFQAGGYLYPQIGDRDL 60
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DB 61 LCPRRAPPGPHSSPNVEFYKLYLVGAQGRCEAPPAVULLTCDPDLDTFTTKFQRY 120
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DB 121 SPNLWHERSHHDYIITATSDGTREGLESLOGGVCLTRGMKVLRLVGOSPRGGAVERP 180
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DB 181 VSEMPMERDRGAHSLIEPKENLPDPTSNATSRGAEGLPPSPMPAVAGAAGLALLL 240
QY 241 GVAAGAGAMCWRRRRAKPSBSRHPGSGFRGGSGLGCGGCGMPREAPBELGIALRGG 300
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DB 241 GVAAGAGAMCWRRRRAKPSBSRHPGSGFRGGSGLGCGGCGMPREAPBELGIALRGG 300
QY 301 GAADPPFCPHYEKVSGDYGHPIYIVODGPPOSPPNIYKYV 340
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DB 301 GAADPPFCPHYEKVSGDYGHPIYIVODGPPOSPPNIYKYV 340
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RESULT 3
US-10-698-907-16
/ Sequence 16, Application US/10698907
/ Publication No. US20050049194A1
/ GENERAL INFORMATION:
/ APPLICANT: Friesen, Jonas
/ APPLICANT: Holmberg, Johan
/ TITLE OF INVENTION: Use of Ephrins and Related Molecules to Regulate Cellular
/ FILE REFERENCE: 21882-529 UTIL
/ CURRENT APPLICATION NUMBER: US/10/698,907
/ PRIOR FILING DATE: 2003-10-31
/ PRIOR APPLICATION NUMBER: US 60/460,488
/ PRIOR FILING DATE: 2003-04-03
/ PRIOR APPLICATION NUMBER: US 10/291,290
/ PRIOR FILING DATE: 2002-11-08
/ PRIOR APPLICATION NUMBER: US 60/393,272
/ PRIOR FILING DATE: 2002-07-02
/ PRIOR APPLICATION NUMBER: US 60/345,206
/ PRIOR FILING DATE: 2001-11-09
/ NUMBER OF SEQ ID NOS: 25
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 16
/ LENGTH: 340
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-698-907-16
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Query Match 100.0%; Score 1850; DB 5; Length 340;
Best Local Similarity 100.0%; Pred. No. 3.5e-131;
Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MGPPHSGPGGVVVGALLLGLVGLVSGLSLEPVYVNSANKRFQAGGYLYPQIGDRDL 60
QY 61 LCPRRAPPGPHSSPNVEFYKLYLVGAQGRCEAPPAVULLTCDPDLDTFTTKFQRY 120
| | | | |
DB 61 LCPRRAPPGPHSSPNVEFYKLYLVGAQGRCEAPPAVULLTCDPDLDTFTTKFQRY 120
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DB 121 SPNLWHERSHHDYIITATSDGTREGLESLOGGVCLTRGMKVLRLVGOSPRGGAVERP 180
QY 181 VSEMPMERDRGAHSLIEPKENLPDPTSNATSRGAEGLPPSPMPAVAGAAGLALLL 240
| | | | |
DB 181 VSEMPMERDRGAHSLIEPKENLPDPTSNATSRGAEGLPPSPMPAVAGAAGLALLL 240
QY 241 GVAAGAGAMCWRRRRAKPSBSRHPGSGFRGGSGLGCGGCGMPREAPBELGIALRGG 300
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DB 241 GVAAGAGAMCWRRRRAKPSBSRHPGSGFRGGSGLGCGGCGMPREAPBELGIALRGG 300
QY 301 GAADPPFCPHYEKVSGDYGHPIYIVODGPPOSPPNIYKYV 340
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DB 301 GAADPPFCPHYEKVSGDYGHPIYIVODGPPOSPPNIYKYV 340
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RESULT 4
US-10-138-787-3
/ Sequence 3, Application US/10138787
/ Publication No. US20020172984A1
/ GENERAL INFORMATION:
/ APPLICANT: Holland, Sacha
/ APPLICANT: Mbamalu, Geraldine
/ APPLICANT: Pawson, Tony
/ TITLE OF INVENTION: OLIGOMERIZED RECEPTORS WHICH AFFECT PATHWAYS REGULATED
/ FILE REFERENCE: 11757.23USMO
/ CURRENT APPLICATION NUMBER: US/10/138,787
/ PRIOR FILING DATE: 2002-05-03
/ PRIOR APPLICATION NUMBER: US/09/214,631
/ PRIOR FILING DATE: 1999-03-12
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;; PRIOR APPLICATION NUMBER: PCT/CA97/00473
;; PRIOR FILING DATE: 1997-07-04
;; PRIOR APPLICATION NUMBER: 60/021,272
;; PRIOR FILING DATE: 1996-07-05
;; NUMBER OF SEQ ID NOS: 13
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 3
;; LENGTH: 340
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-138-787-3

Query Match 99.8%; Score 1846; DB 4; Length 340;
Best Local Similarity 99.7%; Pred. No. 7e-131;
Matches 339; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGPHSGPGGVRRGALLLLGLVGLVSGLSLEPYWNSANKRFOAEGGYLYPQIGRLDL 60
DB 1 MGPHSGPGGVRRGALLLLGLVGLVSGLSLEPYWNSANKRFOAEGGYLYPQIGRLDL 60
QY 61 LCPRARPPGSHSPNTEFYKLYLVGAQGRCAAPAPNLLTCDPDLRLFTIKFOEY 120
DB 61 LCPRARPPGSHSPNTEFYKLYLVGAQGRCAAPAPNLLTCDPDLRLFTIKFOEY 120
QY 121 SPNLMGHEFRSHHDYIIATSDGTREGLESIOGVCILTRGMKYLRLVGOSPRGAVPRKP 180
DB 121 SPNLMGHEFRSHHDYIIATSDGTREGLESIOGVCILTRGMKYLRLVGOSPRGAVPRKP 180
QY 181 VSEMPERDRGAHSLPEKGNLPGDPTSNATSRGAEGLPPSPMPAVAGAAGLALLL 240
DB 181 VSEMPERDRGAHSLPEKGNLPGDPTSNATSRGAEGLPPSPMPAVAGAAGLALLL 240
QY 241 GVAGAGAMCWRARRAKPSRSRHPGSGFRGGSILGIGGGGMPREAEFGELIALRG 300
DB 241 GVAGAGAMCWRARRAKPSRSRHPGSGFRGGSILGIGGGGMPREAEFGELIALRG 300
QY 301 GAADPPCPHYEKVSGDYGHPIYIVODGPPQSPNIIYKYV 340
DB 301 GAADPPCPHYEKVSGDYGHPIYIVODGPPQSPNIIYKYV 340

RESULT 5
US-10-417-924A-2
;; Sequence 2, Application US/10417924A
;; Publication No. US20030215918A1
;; GENERAL INFORMATION:
;; APPLICANT: Samuel Davis, et al.
;; TITLE OF INVENTION: BIOLOGICALLY ACTIVE EPH FAMILY LIGANDS
;; FILE REFERENCE: REG-3412
;; CURRENT APPLICATION NUMBER: US/10/417, 924A
;; PRIOR FILING DATE: 2003-04-17
;; PRIOR APPLICATION NUMBER: 09/051,994
;; PRIOR FILING DATE: 1998-04-24
;; PRIOR APPLICATION NUMBER: PCT/US96/17201
;; PRIOR FILING DATE: 1996-10-25
;; PRIOR APPLICATION NUMBER: 60/007,015
;; PRIOR FILING DATE: 1995-10-25
;; NUMBER OF SEQ ID NOS: 3
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 2
;; LENGTH: 340
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: Misc. feature
;; LOCATION: (166)
;; OTHER INFORMATION: Xaa = unknown or other
US-10-417-924A-2

Query Match 99.7%; Score 1844; DB 4; Length 340;
Best Local Similarity 99.7%; Pred. No. 9.9e-111;
Matches 339; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGPHSGPGGVRRGALLLLGLVGLVSGLSLEPYWNSANKRFOAEGGYLYPQIGRLDL 60
DB 1 MGPHSGPGGVRRGALLLLGLVGLVSGLSLEPYWNSANKRFOAEGGYLYPQIGRLDL 60
QY 61 LCPRARPPGSHSPNTEFYKLYLVGAQGRCAAPAPNLLTCDPDLRLFTIKFOEY 120
DB 61 LCPRARPPGSHSPNTEFYKLYLVGAQGRCAAPAPNLLTCDPDLRLFTIKFOEY 120
QY 121 SPNLMGHEFRSHHDYIIATSDGTREGLESIOGVCILTRGMKYLRLVGOSPRGAVPRKP 180
DB 121 SPNLMGHEFRSHHDYIIATSDGTREGLESIOGVCILTRGMKYLRLVGOSPRGAVPRKP 180
QY 181 VSEMPERDRGAHSLPEKGNLPGDPTSNATSRGAEGLPPSPMPAVAGAAGLALLL 240
DB 181 VSEMPERDRGAHSLPEKGNLPGDPTSNATSRGAEGLPPSPMPAVAGAAGLALLL 240
QY 241 GVAGAGAMCWRARRAKPSRSRHPGSGFRGGSILGIGGGGMPREAEFGELIALRG 300
DB 241 GVAGAGAMCWRARRAKPSRSRHPGSGFRGGSILGIGGGGMPREAEFGELIALRG 300
QY 301 GAADPPCPHYEKVSGDYGHPIYIVODGPPQSPNIIYKYV 340
DB 301 GAADPPCPHYEKVSGDYGHPIYIVODGPPQSPNIIYKYV 340

RESULT 6
US-10-021-121-2
;; Sequence 2, Application US/10021121
;; Publication No. US2002014244A1
;; GENERAL INFORMATION:
;; APPLICANT: Caras, Ingrid W
;; TITLE OF INVENTION: A2-1 Neurotrophic Factor
;; NUMBER OF SEQUENCES: 10
;; CORRESPONDENCE ADDRESS:
;; ADDRESSER: Genentech, Inc.
;; STREET: 1 DNA Way
;; CITY: South San Francisco
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94080
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: WinPatIn (Genentech)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/10/021,121
;; FILING DATE: 06-Dec-2001
;; CLASSIFICATION: <Unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/635,130
;; FILING DATE: 19-Mar-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Torchia, Ph.D., Timothy E.
;; REGISTRATION NUMBER: 36,700
;; REFERENCE/DOCKET NUMBER: P1001
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 650/225-8674
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 455 amino acids
;; TYPE: Amino Acid
;; TOPOLOGY: Linear
;; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-021-121-2

Query Match 99.5%; Score 1841; DB 4; Length 455;
Best Local Similarity 100.0%; Pred. No. 2.3e-130;
Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGPHSGPGGVRRGALLLLGLVGLVSGLSLEPYWNSANKRFOAEGGYLYPQIGRLDL 60

Db 1 MGPBHSFGSVRVGALLLGLVGLVSGLSLEPYWMSANKRFOAEGGYLVYPOIGRLDL 60
QY 1 LCPRAAPPGHSSPNTEFFYKLYLVGAQGRRCAPAPANNLLTCDRPPDLDRFTIKFOEX 120
Db 61 LCPRAAPPGHSSPNTEFFYKLYLVGAQGRRCAPAPANNLLTCDRPPDLDRFTIKFOEX 120
QY 121 SPNLMGHEFRSHHDYIATSDGTREGLESLOGGVCLTRGMKYLRLVGOSSPRGAVPRKP 180
Db 121 SPNLMGHEFRSHHDYIATSDGTREGLESLOGGVCLTRGMKYLRLVGOSSPRGAVPRKP 180
QY 181 VSMEMPERDGAHSLPEKENTLPGDPTSNATSRGAEGLPPSPMPAVAGAAGLALLLL 240
Db 181 VSMEMPERDGAHSLPEKENTLPGDPTSNATSRGAEGLPPSPMPAVAGAAGLALLLL 240
QY 241 GVAGAGGAMCWRRRRAKPSERHPPGSGFGRGSLGLGGGGMGPREAEFGELGIALRG 300
Db 241 GVAGAGGAMCWRRRRAKPSERHPPGSGFGRGSLGLGGGGMGPREAEFGELGIALRG 300
QY 301 GAADPPFCPHYEKVSGDYGHPIYIVODGPPQSPNNIYK 338
Db 301 GAADPPFCPHYEKVSGDYGHPIYIVODGPPQSPNNIYK 338

RESULT 7
US-10-698-907-8
; Sequence 8, Application US/10698907
; Publication No. US20050049194A1
; GENERAL INFORMATION:
; APPLICANT: Friesen, Jonas
; APPLICANT: Holmberg, Johan
; TITLE OF INVENTION: Use of Ephrins and Related Molecules to Regulate Cellular
; FILE REFERENCE: 21882-529 UTIL
; CURRENT APPLICATION NUMBER: US/10/698,907
; CURRENT FILING DATE: 2003-10-31
; PRIOR APPLICATION NUMBER: US 60/460,488
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: US 10/291,290
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: US 60/393,272
; PRIOR FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US 60/345,206
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 340
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-698-907-8

Query Match 96.2%; Score 1780; DB 5; Length 340;
Best Local Similarity 95.6%; Pred. No. 6.6e-126;
Matches 345; Conservative 7; Mismatches 8; Indels 0; Gaps 0;
QY 1 MGPBHSFGSVRVGALLLGLVGLVSGLSLEPYWMSANKRFOAEGGYLVYPOIGRLDL 60
Db 1 MGPBHSFGSVRVGALLLGLVGLVSGLSLEPYWMSANKRFOAEGGYLVYPOIGRLDL 60
QY 61 LCPRAAPPGHSSPNTEFFYKLYLVGAQGRRCAPAPANNLLTCDRPPDLDRFTIKFOEX 120
Db 61 LCPRAAPPGHSSPNTEFFYKLYLVGAQGRRCAPAPANNLLTCDRPPDLDRFTIKFOEX 120
QY 121 SPNLMGHEFRSHHDYIATSDGTREGLESLOGGVCLTRGMKYLRLVGOSSPRGAVPRKP 180
Db 121 SPNLMGHEFRSHHDYIATSDGTREGLESLOGGVCLTRGMKYLRLVGOSSPRGAVPRKP 180
QY 181 VSMEMPERDGAHSLPEKENTLPGDPTSNATSRGAEGLPPSPMPAVAGAAGLALLLL 240
Db 181 VSMEMPERDGAHSLPEKENTLPGDPTSNATSRGAEGLPPSPMPAVAGAAGLALLLL 240
QY 241 GVAGAGGAMCWRRRRAKPSERHPPGSGFGRGSLGLGGGGMGPREAEFGELGIALRG 300
Db 241 GVAGAGGAMCWRRRRAKPSERHPPGSGFGRGSLGLGGGGMGPREAEFGELGIALRG 300

Db 241 GVAGAGGAMCWRRRRAKPSERHPPGSGFGRGSLGLGGGGMGPREAEFGELGIALRG 300
QY 301 GAADPPFCPHYEKVSGDYGHPIYIVODGPPQSPNNIYK 340
Db 301 GAADPPFCPHYEKVSGDYGHPIYIVODGPPQSPNNIYK 340

RESULT 8
US-10-408-765A-2695
; Sequence 2695, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088, 465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2695
; LENGTH: 285
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-2695

Query Match 84.3%; Score 1559; DB 4; Length 285;
Best Local Similarity 100.0%; Pred. No. 2.4e-109;
Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 56 DRDLICPRAPPGHSSPNTEFFYKLYLVGAQGRRCAPAPANNLLTCDRPPDLDRFTI 115
Db 1 DRDLICPRAPPGHSSPNTEFFYKLYLVGAQGRRCAPAPANNLLTCDRPPDLDRFTI 60
QY 116 KFOEYSPNLMGHEFRSHHDYIATSDGTREGLESLOGGVCLTRGMKYLRLVGOSSPRGA 175
Db 61 KFOEYSPNLMGHEFRSHHDYIATSDGTREGLESLOGGVCLTRGMKYLRLVGOSSPRGA 120
QY 176 VPRKPYSEMPERDGAHSLPEKENTLPGDPTSNATSRGAEGLPPSPMPAVAGAAGL 235
Db 121 VPRKPYSEMPERDGAHSLPEKENTLPGDPTSNATSRGAEGLPPSPMPAVAGAAGL 180
QY 236 ALLLGVAGAGGAMCWRRRRAKPSERHPPGSGFGRGSLGLGGGGMGPREAEFGELGI 295
Db 181 ALLLGVAGAGGAMCWRRRRAKPSERHPPGSGFGRGSLGLGGGGMGPREAEFGELGI 240
QY 296 ALRGGAADPPFCPHYEKVSGDYGHPIYIVODGPPQSPNNIYK 340
Db 241 ALRGGAADPPFCPHYEKVSGDYGHPIYIVODGPPQSPNNIYK 285

RESULT 9
US-10-698-907-7
; Sequence 7, Application US/10698907
; Publication No. US20050049194A1
; GENERAL INFORMATION:
; APPLICANT: Friesen, Jonas
; APPLICANT: Holmberg, Johan
; TITLE OF INVENTION: Use of Ephrins and Related Molecules to Regulate Cellular
; FILE REFERENCE: 21882-529 UTIL
; CURRENT APPLICATION NUMBER: US/10/698,907
; CURRENT FILING DATE: 2003-10-31
; PRIOR APPLICATION NUMBER: US 60/460,488
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: US 10/291,290
; PRIOR FILING DATE: 2002-11-08

PRIOR APPLICATION NUMBER: US 60/393,272
PRIOR FILING DATE: 2002-07-02
PRIOR APPLICATION NUMBER: US 60/345,206
PRIOR FILING DATE: 2001-11-09
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patent in version 3.2
SEQ ID NO: 7
LENGTH: 336
TYPE: PRT
ORGANISM: Mus musculus
US-10-698-907-7

Query Match 34.5%; Score 637.5; DB 5; Length 336;
Best Local Similarity 42.1%; Pred. No. 8e-40;
Matches 139; Conservative 49; Mismatches 129; Indels 13; Gaps 5;

QY 14 GALLLLGVLVGLSLPEVYVNSANKRFOAGGYLVYPOIGDRDLCLPRARPPGPHSS 73
DB 17 GLAMVLCRAISRSLVLEIYVNSNSKFLPGQGLVLYPOIGDKLDIICPKV---DSKTV 73
QY 74 PNYEYKVLVVGAGRCRCAPAPNLLTCDRPDLARFTIKFOEYSPNLMGHERSHH 133
DB 74 GQYEVYKVMVMDQADRCTIKKENTPLNLCARPDQVKTTFIKFOEYSPNLMGHERSHH 133
QY 134 DYYIATSDGTREGLESLOGVCLTRGMKVLKRVGO--SPRGAVPRKPVSEMPMR-DR 190
DB 134 DYYIISTSGSLGDLNQGVCQTRAMKILMKVGODASASARHNGFTTRPELEAGTN 193
QY 191 GAHSLPEKENVPGDPTSNATSRGAEGLPPSPMBAVAGAGLALLLVAGAGAGAMC 250
DB 194 GSSSTTSPVKPNPGSSTDGNAGHSGNNLLGSEVALFAGIASGCIIFVITITVLL 253
QY 251 WRRRAKESSEHHPGSGFRGSLGLGGGGMKPRAPGELIALRGGAADPPFCRH 310
DB 254 KYRRHRKRKSPHHTTTLSTLATPRGKGN---NGSEPSDVIIPLR---TADSVFCRH 306
QY 311 YEKVSDYGHVYIVODGPSPSPNYKYK 340
DB 307 YEKVSDYGHVYIVQEMPSPANIYKYK 336

RESULT 10
US-10-021-121-9
Sequence 9, Application US/10021121
Publication No. US2002014244A1
GENERAL INFORMATION:
APPLICANT: Caras, Ingrid W
TITLE OF INVENTION: A2-1 Neurotrophic Factor
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/021,121
FILING DATE: 06-Dec-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/635,130
FILING DATE: 19-Mar-1996
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, PhD., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1001
TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 346 amino acids
TYPE: Amino acids
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-021-121-9

Query Match 34.2%; Score 632; DB 4; Length 346;
Best Local Similarity 39.5%; Pred. No. 2.2e-39;
Matches 145; Conservative 48; Mismatches 116; Indels 58; Gaps 9;

QY 8 PGVAVGALLLVGLVSGL-----SLPEYVNSANKRFOAGGYLVYPOIGDRDL 61
DB 4 PGQRMGLKVLVAVVWALCRLATPLAKNLEPVSWSLNFKLSGKLVYPKIGDKLDII 63
QY 62 CPRARPPGPHSSPNVEFYLVYVGAGRCRCAPAPNLLTCDRPDLARFTIKFOEYS 121
DB 64 CPRAEAGR-----YEVYKVLVVRPQAAACSTVLDPNVLVTCNRPQEIIRFTIKFOEYS 118
QY 122 PVLWGHFRSHHDYIITATSDGTREGLESLOGVCLTRGMKVLKRVGSPRGAVPRKRV 181
DB 119 PVMGLFEFKHHDYITSTNSGSLGLENRREGVCRTRFMKIMKVGODPNVATDEQLTT 178
QY 182 SMPMERDRGAHSLP-PEKENVPGDPTSNATSRGAEGLPPSPMBAVAGAGLA---- 236
DB 179 SRPSKADVTVMQVQAPRSGLSDSDGKHETVNOEKSQP-----GASGGSSGDPD 231
QY 237 -----LALLVAGAGAG-----MWRERRAKPESSEHHPGSGFRGSLGL 277
DB 232 GFPSKVALFAVAGACVIFLLIIFLYVLLKAKRHKHQ-----RAAAL 282
QY 278 -----GGGGMGPRAPGELIALRGGAADPPFCPHYKVSVDYGHVYIVODGPSP 333
DB 283 STLAPKGGSGTAGTEPSDIIIPLR---TTENNYCPHYKVSVDYGHVYIVQEMPSPSP 339
QY 334 ENIYKYK 340
DB 340 ANIYKYK 346

RESULT 11
US-10-356-289-2
Sequence 2, Application US/10356289
Publication No. US20040022767A1
GENERAL INFORMATION:
APPLICANT: Lyman, Stewart D.
APPLICANT: Beckmann, M. Patricia
APPLICANT: Baum, Peter R.
APPLICANT: Carpenter, Melissa K.
TITLE OF INVENTION: NOVEL CYTOKINE DESIGNATED ELK LIGAND
FILE REFERENCE: GENENT.67CPDV3
CURRENT APPLICATION NUMBER: US/10/356,289
FILING DATE: 2003-01-31
PRIOR APPLICATION NUMBER: US/09/039,642B
PRIOR FILING DATE: 1998-03-16
PRIOR APPLICATION NUMBER: 08/213,403
PRIOR FILING DATE: 1994-03-15
PRIOR APPLICATION NUMBER: 07/977,693
PRIOR FILING DATE: 1992-11-13
PRIOR APPLICATION NUMBER: 08/747,240
PRIOR FILING DATE: 1996-10-12
PRIOR APPLICATION NUMBER: 08/460,741
PRIOR FILING DATE: 1995-06-02
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 346
TYPE: PRT
ORGANISM: Homo sapiens
US-10-356-289-2

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Query Match 34.2%; Score 632; DB 4; Length 346;
Beet Local Similarity 39.5%; Pred. No. 2.2e-39;
Matches 145; Conservative 48; Mismatches 116; Indels 58; Gaps 9;

QY 8 PGGVVGAALLLGGVGLVSGL-----SLEPYVMSANKRFOAEGGYLYVPOIGRDLTL 61
DB 4 PQQRWLGKVLVAMVWVALCRLATPLAKNLEPVSWSLNPKFLSGKGLVYIPKIGDKLDII 63
QY 62 CPRARPPGPHSSPNYEFYKLYLVGAQGRCEAPAPNLLTCDRBDLDRFTIKFOEYS 121
DB 64 CPRAEAGR-----YEYKLYLVPRPGAACSTVLDPNVLTVCNRPBGIRFTIKFOEYS 118
QY 122 PWLMGHEFSHDDYIIATSDGTREGLESLOGVCITRGKVLKLVGSGPRGAVPRKRV 181
DB 119 PNYMGLEFKKHDDYITSTNGSLBGLENREGVCRTITMKIMKVGDPNPAVTPEQLTT 178
QY 182 SEMPERDRGAHSLP-PEKENLPGDPTSNATSRGAEGPLPPSPMAVAGAAGLA---- 236
DB 179 SRPSKEADNTVYMAQOAPGSGSLGSDGKHETVNOEKS GP-----GASGSSGDPD 231

RESULT 12
US-10-712-124-60
; Sequence 60, Application US/10712124
; Publication No. US20040146907A1
; GENERAL INFORMATION:
; APPLICANT: SMITH, VICTORIA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING DYSPLASIA
; FILE REFERENCE: P2000R1
; CURRENT APPLICATION NUMBER: US/10/712,124
; PRIOR FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/425, 813
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 123
; SEQ ID NO 60
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-712-124-60

Query Match 34.2%; Score 632; DB 4; Length 346;
Beet Local Similarity 39.5%; Pred. No. 2.2e-39;
Matches 145; Conservative 48; Mismatches 116; Indels 58; Gaps 9;

QY 8 PGGVVGAALLLGGVGLVSGL-----SLEPYVMSANKRFOAEGGYLYVPOIGRDLTL 61
DB 4 PQQRWLGKVLVAMVWVALCRLATPLAKNLEPVSWSLNPKFLSGKGLVYIPKIGDKLDII 63
QY 62 CPRARPPGPHSSPNYEFYKLYLVGAQGRCEAPAPNLLTCDRBDLDRFTIKFOEYS 121
DB 64 CPRAEAGR-----YEYKLYLVPRPGAACSTVLDPNVLTVCNRPBGIRFTIKFOEYS 118
QY 122 PWLMGHEFSHDDYIIATSDGTREGLESLOGVCITRGKVLKLVGSGPRGAVPRKRV 181
DB 119 PNYMGLEFKKHDDYITSTNGSLBGLENREGVCRTITMKIMKVGDPNPAVTPEQLTT 178
QY 182 SEMPERDRGAHSLP-PEKENLPGDPTSNATSRGAEGPLPPSPMAVAGAAGLA---- 236
DB 179 SRPSKEADNTVYMAQOAPGSGSLGSDGKHETVNOEKS GP-----GASGSSGDPD 231
```

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QY 237 -----LILLGVAAGGA-----MCWRRRAKPSSESHHPGSGFRGSGSLG 277
DB 232 GFENSKVALFAAVGAGCVIFLLIIFLTVLKLRKRRKHQO-----RAAALSL 282
QY 278 -----GGGGMGPRAEPBELGIALRGGAADPPFCPHYEKVSGDGHPIYIVODGPPOSP 333
DB 283 STLASPKGSGGTAGTEPSDIIIPLR---TTENNVCPHYEKVSGDGHPIYIVODGPPOSP 339

QY 334 PNIYKVV 340
DB 340 ANIYKVV 346

RESULT 13
US-10-789-378-30
; Sequence 30, Application US/10789378
; Publication No. US20050003390A1
; GENERAL INFORMATION:
; APPLICANT: Akenovich, Sergey
; APPLICANT: Stull, Robert
; APPLICANT: Gelman, Marina
; APPLICANT: Chui, Kitya
; APPLICANT: Ng, Dean
; TITLE OF INVENTION: DIAGNOSTIC METHODS FOR CANCER DETECTION
; FILE REFERENCE: 5189-2
; CURRENT APPLICATION NUMBER: US/10/789,378
; PRIOR FILING DATE: 2004-02-26
; PRIOR APPLICATION NUMBER: 10/441925
; PRIOR FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: 60/381619
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/450886
; PRIOR FILING DATE: 2003-02-26
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.1.1
; SEQ ID NO 30
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-789-378-30

Query Match 34.2%; Score 632; DB 5; Length 346;
Beet Local Similarity 39.5%; Pred. No. 2.2e-39;
Matches 145; Conservative 48; Mismatches 116; Indels 58; Gaps 9;

QY 8 PGGVVGAALLLGGVGLVSGL-----SLEPYVMSANKRFOAEGGYLYVPOIGRDLTL 61
DB 4 PQQRWLGKVLVAMVWVALCRLATPLAKNLEPVSWSLNPKFLSGKGLVYIPKIGDKLDII 63
QY 62 CPRARPPGPHSSPNYEFYKLYLVGAQGRCEAPAPNLLTCDRBDLDRFTIKFOEYS 121
DB 64 CPRAEAGR-----YEYKLYLVPRPGAACSTVLDPNVLTVCNRPBGIRFTIKFOEYS 118
QY 122 PWLMGHEFSHDDYIIATSDGTREGLESLOGVCITRGKVLKLVGSGPRGAVPRKRV 181
DB 119 PNYMGLEFKKHDDYITSTNGSLBGLENREGVCRTITMKIMKVGDPNPAVTPEQLTT 178
QY 182 SEMPERDRGAHSLP-PEKENLPGDPTSNATSRGAEGPLPPSPMAVAGAAGLA---- 236
DB 179 SRPSKEADNTVYMAQOAPGSGSLGSDGKHETVNOEKS GP-----GASGSSGDPD 231

QY 237 -----LILLGVAAGGA-----MCWRRRAKPSSESHHPGSGFRGSGSLG 277
DB 232 GFENSKVALFAAVGAGCVIFLLIIFLTVLKLRKRRKHQO-----RAAALSL 282
QY 278 -----GGGGMGPRAEPBELGIALRGGAADPPFCPHYEKVSGDGHPIYIVODGPPOSP 333
DB 283 STLASPKGSGGTAGTEPSDIIIPLR---TTENNVCPHYEKVSGDGHPIYIVODGPPOSP 339

QY 334 PNIYKVV 340
DB 340 ANIYKVV 346
```


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OM protein - protein search, using sw model

Run on: December 21, 2005, 14:36:40 ; Search time 6.41509 Seconds
(without alignments)
378.002 Million cell updates/sec

Title: US-10-021-121-4

Perfect score: 1850

Sequence: 1 MGPSPHSGPGRVAGALLLG.....PVYIVQDPGPPQSPNNIYKV 340

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 53982 seqs, 7132107 residues

Total number of hits satisfying chosen parameters: 53982

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:
1: /cgn2_6/prodata/2/pubpaa/US08_NEW_PUB pep.*
2: /cgn2_6/prodata/2/pubpaa/US06_NEW_PUB pep.*
3: /cgn2_6/prodata/2/pubpaa/US07_NEW_PUB pep.*
4: /cgn2_6/prodata/2/pubpaa/FCF_NEW_PUB pep.*
5: /cgn2_6/prodata/2/pubpaa/US09_NEW_PUB pep.*
6: /cgn2_6/prodata/2/pubpaa/US10_NEW_PUB pep.*
7: /cgn2_6/prodata/2/pubpaa/US11_NEW_PUB pep.*
8: /cgn2_6/prodata/2/pubpaa/US60_NEW_PUB pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	629.5	34.0	333	US-10-949-720-396	Sequence 396, App
2	446.5	24.1	459	US-10-949-720-390	Sequence 390, App
3	442	23.9	233	US-10-949-720-388	Sequence 388, App
4	164.5	8.9	204	US-10-131-826A-288	Sequence 288, App
5	144.5	7.8	1516	US-10-220-824-8	Sequence 8, App1
6	142.5	7.7	1496	US-11-186-284-35	Sequence 35, App1
7	142	7.7	744	US-11-186-284-37	Sequence 37, App1
8	142	7.7	744	US-11-186-284-39	Sequence 39, App1
9	141.5	7.6	1166	US-10-821-234-964	Sequence 964, App
10	141.5	7.6	1466	US-11-186-284-33	Sequence 33, App
11	137.5	7.4	1874	US-10-821-234-1182	Sequence 1182, App
12	135.5	7.3	1532	US-10-821-234-914	Sequence 914, App
13	134.5	7.3	1366	US-10-821-234-1431	Sequence 1431, App
14	134.5	7.3	1366	US-11-186-284-31	Sequence 31, App1
15	133	7.2	1464	US-11-186-284-28	Sequence 28, App1
16	133	7.2	1464	US-10-821-234-1096	Sequence 1096, App
17	132	7.1	1464	US-11-000-463-243	Sequence 243, App
18	129	7.0	1767	US-10-995-561-911	Sequence 911, App
19	129	7.0	1767	US-10-995-561-914	Sequence 914, App
20	129	7.0	1806	US-10-995-561-912	Sequence 912, App
21	129	7.0	1806	US-10-995-561-915	Sequence 915, App
22	129	7.0	1818	US-10-995-561-910	Sequence 910, App
23	129	7.0	1818	US-10-995-561-913	Sequence 913, App
24	126.5	6.8	520	US-10-995-561-532	Sequence 532, App
25	123	6.6	3063	US-11-186-284-26	Sequence 26, App1

26	116.5	6.3	1823	6	US-10-995-561-988	Sequence 988, App
27	116.5	6.3	2102	6	US-10-995-561-990	Sequence 990, App
28	116.5	6.3	2108	6	US-10-995-561-989	Sequence 989, App
29	116.5	6.3	2157	6	US-10-995-561-991	Sequence 991, App
30	114	6.2	828	6	US-10-995-561-983	Sequence 983, App
31	114	6.2	918	6	US-10-995-561-981	Sequence 981, App
32	114	6.2	1019	6	US-10-995-561-982	Sequence 982, App
33	113.5	6.1	580	6	US-10-995-561-987	Sequence 987, App
34	112	6.1	924	6	US-10-857-780-20	Sequence 20, App1
35	111	6.0	641	6	US-10-848-976-1	Sequence 1, App1
36	107	5.8	924	7	US-11-107-028-26	Sequence 26, App1
37	104.5	5.6	244	6	US-10-477-507A-4	Sequence 4, App1
38	104.5	5.6	456	6	US-10-477-507A-2	Sequence 2, App1
39	104.5	5.6	467	6	US-10-821-234-1688	Sequence 1688, App
40	103.5	5.6	884	6	US-10-995-561-786	Sequence 786, App
41	102	5.5	119	7	US-11-110-424-4	Sequence 4, App1
42	101.5	5.5	673	7	US-11-102-240-16	Sequence 16, App1
43	99.5	5.4	368	7	US-11-085-775-3	Sequence 3, App1
44	99	5.4	318	6	US-10-802-796-727	Sequence 727, App
45	99	5.4	334	6	US-10-802-796-728	Sequence 728, App

ALIGNMENTS

RESULT 1
US-10-949-720-396
; Sequence 396, Application US/10949720
; Publication No. US20050249736A1
; GENERAL INFORMATION:
; APPLICANT: Krasnoperov, Valery
; APPLICANT: Zozulya, Sergey
; APPLICANT: Kertesz, Mathalie
; APPLICANT: Reddy, Ramachandra
; APPLICANT: G111, Parakash
; TITLE OF INVENTION: POLYPEPTIDE COMPOUNDS FOR INHIBITING
; FILE REFERENCE: VASG-P02-002
; CURRENT APPLICATION NUMBER: US/10/949,720
; CURRENT FILING DATE: 2004-09-23
; PRIOR APPLICATION NUMBER: US 60/454,432
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 60/454,300
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/800,350
; PRIOR FILING DATE: 2004-03-12
; NUMBER OF SEQ ID NOS: 425
; SOFTWARE: FaestSeq for Windows Version 4.0
; SEQ ID NO 396
; LENGTH: 333
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-949-720-396
Query Match 34.0%; Score 629.5; DB 6; Length 333;
Best local Similarity 40.9%; Pred. No. 1,7e+42;
Matches 135; Conservative 52; Mismatches 130; Indels 13; Gaps 5;
QY 14 GALLLVGLVSGLSLEPVNWSANKRPOAEGVYLYPQIDRLDLCPRARPPGPHSS 73
DB 14 GYLVMLCFRAIYSIYLBRIYNNSSNSKFLPQGLVLYPQIDKDIIPKV---DSKTV 70
QY 74 PVNEFYKLYVGAGCRREARPPALLLTCRPRDLARFTTKFOEYSNNMGHEFRSH 133
DB 71 GQVEYKYVMVNDQADRCTTIKENTPILNCAKPPQDIKFTIKFOEYSNNMGLEFQNK 130
QY 134 DVIYIATSGTREGLESLOGVCLTFGMKYLRLVCG--SPRGAVYRKPSVEMPER-DR 190
DB 131 DVIYIATSGTREGLESLOGVCLTFGMKYLRLVCG--SPRGAVYRKPSVEMPER-DR 190
QY 191 GAHSLPEKKNLPGDPTSNATSRGAEGPLPPSPMPVAVGAAGLALLLVGAGAGCANC 250
DB 191 GRSSTTSFVKPNPGSSTGDSNAGHGNILGSEVALFAGIASGCIIFVIITLVLL 250

[illegible]

RESULT 2

```

1      Sequence 390, Application US/10949720
2      Publication No. US20050249736A1
3      GENERAL INFORMATION:
4      APPLICANT: Kraenopetrov, Valery
5      APPLICANT: Zozulya, Sergey
6      APPLICANT: Kertesz, Nathalie
7      APPLICANT: Reddy, Ramachandra
8      APPLICANT: Gill, Parvash
9      TITLE OF INVENTION: POLYPEPTIDE COMPOUNDS FOR INHIBITING
10     TITLE OF INVENTION: ANGIOGENESIS AND TUMOR GROWTH
11     FILE REFERENCE: VASG-P02-002
12     CURRENT APPLICATION NUMBER: US/10/949,720
13     CURRENT FILING DATE: 2004-09-23
14     PRIOR APPLICATION NUMBER: US 60/454,432
15     PRIOR FILING DATE: 2003-03-12
16     PRIOR APPLICATION NUMBER: US 60/454,300
17     PRIOR FILING DATE: 2003-03-12
18     PRIOR APPLICATION NUMBER: US 10/800,350
19     PRIOR FILING DATE: 2004-03-12
20     NUMBER OF SEQ ID NOS: 425
21     SOFTWARE: FastSeq for Windows Version 4.0
22     SEQ ID NO 390
23     LENGTH: 459
24     TYPE: PRT
25     ORGANISM: Unknown
26     FEATURE:
27     OTHER INFORMATION: Recombinant B2EC-FC protein
28     US-10-949-720-390

```

Query Match	24.1%	Score 446.5	DB 6	Length 459
Best Local Similarity	33.7%	Pred. NO. 4.5e-28		
Matches 105, Conservative	39	Mismatches 83	Indels 85	Gaps 7

[illegible]

RESULT 3

US-10-949-720-388
, Sequence 388, Application US/10949720

```

1 # Publication No. US20050249736A1
2 # GENERAL INFORMATION:
3 # APPLICANT: Kravopetrov, Valery
4 # APPLICANT: Zozulya, Sergey
5 # APPLICANT: Kertesz, Nathalie
6 # APPLICANT: Reddy, Ramachandra
7 # APPLICANT: Gill, Patrick
8 # TITLE OF INVENTION: POLYPEPTIDE COMPOUNDS FOR INHIBITING
9 # TITLE OF INVENTION: ANGIOGENESIS AND TUMOR GROWTH
10 # FILE REFERENCE: VASG-P02-002
11 # CURRENT APPLICATION NUMBER: US/10/949,720
12 # CURRENT FILING DATE: 2004-09-23
13 # PRIOR APPLICATION NUMBER: US 60/454,432
14 # PRIOR FILING DATE: 2003-03-12
15 # PRIOR APPLICATION NUMBER: US 60/454,300
16 # PRIOR FILING DATE: 2003-03-12
17 # PRIOR APPLICATION NUMBER: US 10/800,350
18 # PRIOR FILING DATE: 2004-03-12
19 # NUMBER OF SEQ ID NOS: 425
20 # SOFTWARE: PasteSeq for Windows Version 4.0
21 # SEQ ID NO 388
22 # LENGTH: 233
23 # TYPE: PRT
24 # ORGANISM: Unknown
25 # FEATURE:
26 # OTHER INFORMATION: Recombinant B2EC protein
27 # US-10-949-720-388

```

! OTHER INFORMATION: Recombinant B2EC protein
US-10-949-720-388

Query Match	Score	DB	Length
23.9%	442	6	233

Best Local Similarity 35.8%; Pred. NO. 4.7e-28;
Matches 97; Conservative 36; Mismatches 76; Indels 62; Gaps 4;

Qy	1	GALLIGLVIGLVSGISLPEVWNSANKFOAGEGGVLYPOLGIDLLCPAPRPPHSS	73
		14	GVLMVLCRAIKSISVLEPIYWNSSKFLPEGGSLVLPQIGDLDIIICPV--DBKT
Db	14		70
Qy	74	PNVEFYKLVYVGAGQRCGRCAPPAENLLITCDRPLDITIKFOEYSPNIMGHEFRSH	133
		71	GQYEYKVMVKDQADRCTIKKENTPLYNCAKPPODIKFTIKFOEFPNIMGLEPQNK
Db	71		130
Qy	134	DYIIITSDGTREGESLGGGVCILRNGKVLVLRVQSGRGAVPRKPVSEMPMERDRGAA	193
		131	DYIIISTSGELNDQGVGCQIRANKILMKVQ-----
Db	131		166
Qy	194	HSLEPKENLPQDPTSNATSRGABGLRPPSPMAPVAGAAGLALLLVAGAGAMCMRR	253
		167	-----DASSAGSTANKDPTTRPELE-----ACTNG-----
Db	167		191
Qy	254	RRAKPESRHRPGSGRGSGSLGLGGGGMG	284
		192	KSSTTSPPVKNPAGSSTDENSAGHGNNILG
Db	192		222

RESULT 4

US-10-131-826A-288
; Sequence 288, Application US/10131826A
; Publication No. US20050245730A1

APPLICANT:	Baker, Kevin P.
APPLICANT:	Beresini, Maureen
APPLICANT:	Berge, Laura
APPLICANT:	Desnoyers, Luc
APPLICANT:	Filyaroff, Ellen
APPLICANT:	Gao, Wei-Qiang
APPLICANT:	Gerissen, Mary E.
APPLICANT:	Goddard, Audrey
APPLICANT:	Goodman, Paul J.
APPLICANT:	Gurney, Austin L.
APPLICANT:	Shemwood, Steven
APPLICANT:	Smith, Victoria
APPLICANT:	Stewart, Timothy A.
APPLICANT:	Tunas, Daniel
APPLICANT:	Watanabe, Colin K

```

APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C128
CURRENT APPLICATION NUMBER: US/10/131,826A
CURRENT FILING DATE: 2002-04-24
PRIORITY APPLICATION NUMBER: 60/049911
PRIORITY FILING DATE: 1997-06-18
PRIORITY APPLICATION NUMBER: 60/056974
PRIORITY FILING DATE: 1997-08-26
PRIORITY APPLICATION NUMBER: 60/059113
PRIORITY FILING DATE: 1997-09-17
PRIORITY APPLICATION NUMBER: 60/059115
PRIORITY FILING DATE: 1997-09-17
PRIORITY APPLICATION NUMBER: 60/059117
PRIORITY FILING DATE: 1997-09-17
PRIORITY APPLICATION NUMBER: 60/059122
PRIORITY FILING DATE: 1997-09-17
PRIORITY APPLICATION NUMBER: 60/059184
PRIORITY FILING DATE: 1997-09-17
PRIORITY APPLICATION NUMBER: 60/059263
PRIORITY FILING DATE: 1997-09-18
PRIORITY APPLICATION NUMBER: 60/053352
PRIORITY FILING DATE: 1997-09-19
PRIORITY APPLICATION NUMBER: 60/059588
PRIORITY FILING DATE: 1997-09-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 288
LENGTH: 204
TYPE: PRT
ORGANISM: Homo Sapien
IS-10-131-826A-288

```

	Query Match	8.9%	Score 164.5,	DB 6;	Length 204;
	Best Local Similarity	27.7%	Pred No.18e-06;		
	Matches	46;	Conservative	31;	Mismatches 74; Indels 15; Gaps 5.
Oy	18 LLAGVIGLVGSLSEFVVYNNYSANKRFQAGGVLYLPQLDRLDLCPRAPRPGPHSS-PNY	76			
Dd	8 ILGLCCSLLAADRHVTFFWNSSNPKFRNE-DYTIHQWLNDYYDIICPHE---DHSDAAM	63			
Oy	77 EFYULYLVGGAQGRRCEAPRNILLITCDRPDL--DIRFTIKFOEYPNIWGHERSHH	133			
Dd	64 EQYLIVLVEHEHYQLCQPQSXDQYWQCNRPSAKHGPRKLSBKFORFPRTLTGEKEFGKH	123			
Oy	134 DYUFIANSDDTREGESLEQQGVCLTRGGKKVLIRVQSGRGCAVPXK	179			
Dd	124 SYVIISKPIQHEDR-----CLKATVSAGKITHSFDADNPQE	162			

```

RESULT 5
US-10-220-824-8
: Sequence 8, Application US/10720824
: Publication No. US20050277603A1
: GENERAL INFORMATION:
: APPLICANT: Vimedex Limited
: TITLE OF INVENTION: Compositions for gene therapy of rheumatoid arthritis including a
: FILE OF INVENTION: gene encoding an anti-angiogenic protein or parts thereof
: FILE REFERENCE: OPF0208/PCT
: CURRENT APPLICATION NUMBER: US/10/220, 824
: CURRENT FILING DATE: 2002-08-30
: PRIOR APPLICATION NUMBER: KR 2001-0000691
: PRIOR FILING DATE: 2001-01-05
: NUMBER OF SEQ ID NOS: 16
: SOFTWARE: kopatentn 1.771
: SEQ ID NO 8
: LENGTH: 1516
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-220-824-8

```

Query Match	7.8%	Score 144.5	DB 6	Length 1516
Best Local Similarity	23.5%	Pred. No. 0.00062		
Matches	73	Conservative 18	Mismatches 82	Indels 137
			Gaps	15
QY	52	PQIGRDLDLCPRARPPGPHSSPNVYEFKYLVGGAQGRCEARPAEPAWLLTCDRDL	111	
DB	620	PQVGR-----GPGPGQGP-----GPGGFS-----	640	
QY	112	RFTTKFOEYSPNLNGHEFRSHDDYIIATISQTRBG--LESLOGCVCLTKMKLLRVQ	169	
DB	641	-----FR--HDKLTPTIDMGSGGCGDLALRG--	665	
QY	170	SPRGAVPRKP--VSEMERDQGAHSLF--PGKENLPQDDTSNATSGARGPLPSPMP	226	
DB	666	--PRGPGPGPGVPGTLGEBPGRGVNSDVPAGPLGVP-----GRGPGPGPLP	717	
QY	227	AVAGAAGLALLLVAGAGAGAMCWRRRARAPSESRRHPGPGSGFGSGSLGCGCGGMPR	286	
DB	718	GPPGPBG-----RGGPRTQKSGLSGAGAPGHGKS	749	
QY	287	EAEPGELIALRGG-----GAADPPFCP-----HYEKGSGDYGHNPVITV---Q	326	
DB	750	KGAGPGAGARGESGLAGAPGACGPPGPGPPGPGPLPAFGFDMEGS--GGPFWSTARSA	808	
QY	327	DGPPSPENI	336	
DB	809	DG--PQGPGL	817	

```

RESULT 6
US-11-186-284-35
Sequence 35, Application US/11186284
Publication No. US20050266493A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Berger, Allison
APPLICANT: Guillemette, Tracy L.
APPLICANT: Kamatkar, Shubhangi
APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Thibodeau, Stephen N.
APPLICANT: Burgart, Lawrence J.
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
FILE OF INVENTION: THERAPY OF COLON CANCER
FILE REFERENCE: MEM01-0292RRM
CURRENT APPLICATION NUMBER: US/11/186,284
CURRENT FILING DATE: 2005-07-21
PRIOR APPLICATION NUMBER: US/10/301,822
PRIOR FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/381,988
PRIOR FILING DATE: 2002-05-20
NUMBER OF SEQ ID NOS: 228
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 35
LENGTH: 1496
TYPE: PRT
ORGANISM: Homo Sapiens
US-11-186-284-35

```

```
Query Match      7.7%; Score 142.5; DB: 7; Length 1496;  
Best Local Similarity 29.1%; Pred. No. 0.00088;  
Matches 55; Conservative 15; Mismatches 76; Indels 43; Gaps 9;
```

OY 169 QSPFG--GAV-PRKXVSEMPMERDRGAHSLPEKENVLP-----DPSNATSKAG 217
 ||| |
Db 500 RGPFGDPDTGLPPPVBERGAPGNRGF----PSSDLPGCKGAQGERGFVGSSGGPKSQ 554
 ||| |

OY 218 GPLPPSPMPAVAGAAGLALLLLGVAVAGAGCMRRRRARRKSBSRHPP-----GSFGHG 273

```
Db 555 GDBRGEGEGLPGARG-----LTGNPGVGGPEKGLPGALPGDGRPGPPSGTIGKQPG 609
Qy 274 SLGLGGGGMGPBEAPGELGIALRGGAADPPFCPHYKEVSGDYHPPYIIVODGPP--- 330
Db 610 TWGLPPEPKSNPDGKPGFAG-----NPGVPGGARGAKGCKGKCPYGP-----GPPGLR 659
Qy 331 -----QSP 334
Db 660 GEREGEGP 668

RESULT 7
US-11-186-284-37
; Sequence 37, Application US/11186284
; Publication No. US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MPM01-029P2RM
; CURRENT APPLICATION NUMBER: US/11/186,284
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 744
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-186-284-37

Query Match 7.7%; Score 142; DB 7; Length 744;
Best Local Similarity 23.5%; Pred. No. 0.00044;
Matches 73; Conservative 16; Mismatches 96; Indels 126; Gaps 14;

Qy 67 PRGPHSSPNYEFYKYLIVGAAGRCRCEAPAPNLLTLCORPDLRFTIKFGQYSPNLM 126
Db 198 PRGPHGLPG-----IGKPGGPGLPQGPGPK----- 222
Qy 127 HEFRSHHDYIATSDGTREGLSLOGGVCLTRGMKVLIRVGQSPRGAVPRKPVSEMPM 186
Db 223 -----GDRGKGLPGPG-----LRGPKDGKGFGRGAPGVKGP- 256
Qy 187 ERDRGAHSLPEKENTPGDPTSNATG-RGAEGLPPPSMPAVAGAAGLALLL-----G 241
Db 257 -----PGMHGL-PGVGGLPGVKGPGVTGPGPGPLGKPGAPGPRGPGPIGVPGVGP 311
Qy 242 VAGAGGAMCWRRRARAPSESRRHG-----PGSFRGGS 274
Db 312 IPGIG-----KPGDGI PGQPGPGKGEQGLPGLPAGLPGLGKPGFP 361
Qy 275 LGLG-GCGMGPRBEAPGELGIALRGGAADP--PFCPHYKEVSGDYHPPYIIVODGP-- 329
Db 362 RGMGVPALGPR-GEKGPIGSPGIGSGPSPGPGIP-----GPMGPALGFP 414
Qy 330 -----QSP 334
```

```
Db 415 ECGIVPGQGP 425

RESULT 8
US-11-186-284-39
; Sequence 39, Application US/11186284
; Publication No. US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MPM01-029P2RM
; CURRENT APPLICATION NUMBER: US/11/186,284
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 744
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-186-284-39

Query Match 7.7%; Score 142; DB 7; Length 744;
Best Local Similarity 23.3%; Pred. No. 0.00044;
Matches 72; Conservative 16; Mismatches 99; Indels 122; Gaps 13;

Qy 67 PRGPHSSPNYEFYKYLIVGAAGRCRCEAPAPNLLTLCORPDLRFTIKFGQYSPNLM 126
Db 198 PRGPHGLPG-----IGKPGGPGLPQGPGPK----- 222
Qy 127 HEFRSHHDYIATSDGTREGLSLOGGVCLTRGMKVLIRVGQSPRGAVPRKPVSEMPM 186
Db 223 -----GDRGKGLPGPG-----LRGPKDGKGFGRGAPGVKGP- 256
Qy 187 ERDRGAHSLPEKENTPGDPTSNATG-RGAEGLPPPSMPAVAGAAGLALLL-----G 241
Db 257 -----PGMHG-PPGVPGLPGVKGPGVTGPGPGPLGKPGAPGPRGPGPIGVPGVGP 311
Qy 242 VAGAGGAMCWRRRARAPSESRRHG-----PGSFRGGS 274
Db 312 IPGIG-----KPGDGI PGQPGPGKGEQGLPGLPAGLPGLGKPGFP 361
Qy 275 LGLG-GCGMGPRBEAPGELGIALRGGAADP--PFCPHYKEVSGDYHPPYIIVODGP-- 329
Db 362 RGMGVPALGPR-GEKGPIGSPGIGSGPSPGPGIP-----PGEFGLPGIGMPGPRGALGFP 416
Qy 330 -----QSP 334
Db 417 GIVPGQGP 425

RESULT 9
US-10-821-234-964
; Sequence 964, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
```


APPLICANT: Stache-Crain, Birgit
APPLICANT: Andarmant, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pc_seq_genes Version 1.0
SEQ ID NO 964
LENGTH: 1166
TYPE: PRT
ORGANISM: Homo sapiens
US-10-821-234-964

Query Match 7.6%; Score 141.5; DB 6; Length 1166;
Best Local Similarity 28.1%; Pred. No. 0.0008;
Matches 59; Conservative 11; Mismatches 83; Indels 57; Gaps 8;

QY 165 LRVGSP-----RCGAVPRKP-----VSEMPHER-----DRGAHSLPEPK 200
DB 697 LRGAGPPEBEGGKGAAGPPGAAATPGLQMPGRRGLSGSPGKDGK-----EPGG 751
QY 201 ENLPGDPTSNATSRGAEPLPPSPMDPAVAGAG-GLALLLGVAGAGAMCWRRAKPS 259
DB 752 PGADVPFGDG-PRGTPTLGPFGPAQGPEDKKEGAPGLPGIAPRSGSGERGETGPPG 810
QY 260 ESRHPPG-----PGSPRGSLGLGGGGGMPREAREPGLGIALRGGA 303
DB 811 PGAFPAQNGRPGKGERGARGKEGEGSPGVAGPBGDGTSGHPPGIG-----861
QY 304 DPFPCHYEKVSQDYGHPYITVDDPPQSP 333
DB 862 -PFGPRNGRGERSGSPGHPGPQPPGP 890

RESULT 10
US-11-186-284-33
Sequence 33, Application US/1186284
Publication No. US2005026493A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Berger, Allison
APPLICANT: Guillemette, Tracy L.
APPLICANT: Kamatkar, Shubhangi
APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Thibodeau, Stephen N.
APPLICANT: Burgart, Lawrence J.
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
FILE REFERENCE: MPM01-029P2RM
CURRENT APPLICATION NUMBER: US/11/186,284
CURRENT FILING DATE: 2005-07-21
PRIOR APPLICATION NUMBER: US/10/301,822
PRIOR FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/381,988
PRIOR FILING DATE: 2002-05-20
NUMBER OF SEQ ID NOS: 228
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 33
LENGTH: 1466
TYPE: PRT
ORGANISM: Homo Sapiens
US-11-186-284-33

Query Match 7.6%; Score 141.5; DB 7; Length 1466;
Best Local Similarity 27.6%; Pred. No. 0.001;
Matches 61; Conservative 13; Mismatches 74; Indels 73; Gaps 10;

QY 171 PRGAVPRKPVSEMPHERDGA-----AHSLEPKENLPGDPTSNAT-----SRGAG 218
DB 844 PPGSGPAPGPPGQGVKGERGSPGAGAFPGARGLPGPPGSGNPPGPPSGPKDG 903
QY 219 PLPP-----PSMPVAGAAAGL-----ALLLGVAGAGAMCWRRA 256
DB 904 PPGPAGTGAFGSPVSGPRGDAQDPEKSPPAQGPFGAPGLGIGTAGAGLAGPPG 963
QY 257 KPESRHPG-----GSPRGSGSLGCG-GGGMGP-----REAREPGLGIAL 297
DB 964 MPGRGSPGQGVKSGKRGANGLSBERPPGPGGLPGLTAGAPRGRDGNPSDGLPG 1023
QY 298 RGG-----GADPPCHYEKVSQDYGHPYITVDDPP 330
DB 1024 RDGSPGAKDRGKSGSPAG-----GAPGHP-----GPP 1052

RESULT 11
US-10-821-234-1182
Sequence 1182, Application US/10821234
Publication No. US20050255114A1
GENERAL INFORMATION:
APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Andarmant, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pc_seq_genes Version 1.0
SEQ ID NO 1182
LENGTH: 1874
TYPE: PRT
ORGANISM: Homo sapiens
US-10-821-234-1182

Query Match 7.4%; Score 137.5; DB 6; Length 1874;
Best Local Similarity 25.5%; Pred. No. 0.0028;
Matches 79; Conservative 15; Mismatches 85; Indels 131; Gaps 18;

QY 61 LCPRARPPGHSPNTEFYKLVVGAAG-----RRCAPAPNLLTCRPPDL 110
DB 602 LTRPGVPBPQS-----GGLKGPEDVVGPRGVGPFP-----AGRP---642
QY 111 LRETFKQESYPLWGHFRSHHDYIATSDTR-----EGLESIQGV 156
DB 643 -----GRGR-----AGSDARGMPTGTGKDRGFDGLAPG---676
QY 157 LTRGMKVLRLVGSPRGGAVPKRPVSEMPHERDGAHSLPEKENLPGDPTSNATSRGA 216
DB 677 -----EKGNHDPGSPGPPPPGDDGRG--DDGEVPRGLPSP---GPRGL 719
QY 217 EGPLPPSPMDPAVAGAGLALLLGVAGAGAMCWRRAKPSRRAKPSRRA 275
DB 720 LEPKPPGPPGPPGVG-----HDGPRKXNV-----GPGSEPPPPGQGNPAG 765
QY 276 GL-GGGGMPREAREPGLGIALRG-----GAADPPCHYEKVSQDYGHPYITVDDPP 329
DB 766 GLPFGGATGP-----PGEKGPLKRPGLPGMPADGP-----GHP---GKEGP 806
QY 330 P-----QSP 334
DB 807 PGEKGGGPP 816

```
RESULT 12
US-10-821-234-914
; Sequence 914, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmat, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for diagnosis and treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pc_seq_genes Version 1.0
; SEQ ID NO 914
; LENGTH: 1532
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-914

Query Match          7.3%; Score 135.5; DB 6; Length 1532;
Best Local Similarity 23.3%; Pred. No. 0.0032;
Matches 69; Conservative 18; Mismatches 102; Indels 105; Gaps 11;

QY 65 ARPRGHSSPNYEFYKLYLVGAQGR-----CEAPPAENLLTCDRPDLRLTF 117
DB 684 AGRPBPHGPPG-----VPGSVGRKSSGSPGQPPPP----- 716
QY 118 QEVSPNLMGHEFRSHHDYIATSDGTREGLSELOGGVCTTRGMKYLVRVGSPPGAVP 177
DB 717 -----VGLQGLRGEVLP-GVK-----GDKPMGP 740
QY 178 RKEVSEMPMERDGAHSLERPKENLPDPTSNATSRGAEPRLPPSPMAVAGAGLAL 237
DB 741 PGKGPQGEKGRPLNG--EPGMRGLPG-AVGEPAKAKGAPAGPDGHQGRGEQG---- 793
QY 238 LLLGVAGAGAMCWRRRRARPPSSRRPG-PSGRGSGSLGGGGGCMGRPAAPGLGTA 296
DB 794 -LTMGCI-----KGPSPSGDPGKPLGTGPGQPLPTPGAPGIGKGPAGPKI 843
QY 297 LRGGA-----DPPFCPHYEKVSGDYHAPVYIVODGPPSP 333
DB 844 VISEGSSMLTVPRPPRPGAMGPRPGAGAPRAGPLRHNQVNLQGRPPR 897

RESULT 13
US-10-821-234-1431
; Sequence 1431, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmat, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for diagnosis and treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pc_seq_genes Version 1.0
; SEQ ID NO 1431
; LENGTH: 1366
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1431

Query Match          7.3%; Score 134.5; DB 6; Length 1366;
Best Local Similarity 25.3%; Pred. No. 0.0033;
```

```
Matches 89; Conservative 14; Mismatches 114; Indels 135; Gaps 22;

QY 3 PPHSGPGV--RYGALLILGLVGLVSGLSLEPYVWNSANKRFQAEQGYLYPQIGRLDL 60
DB 321 PGLPBRGILPGVGAAGATGARGLVGEPPAPASKESGKSGAGSAG-----PQ----- 369
QY 61 LCPRARPPGHSSPNYEFYKLYLVGAQGR-----CEAPPAENLLTCDRPDLRLTF 113
DB 370 -----GPPGP-----SGEGRKRPNGAGSAGPPG----- 395
QY 114 TIKQEVSPNLMGHEFRSHHDYIATSDGTREGLSELOGGVCTTRGMKYLVRVGSPP 172
DB 396 -----PGLNG-----SPGSR-GLPGADG-----RAGMGPP 420
QY 173 GGAVPKPVSEMPMERDGAHSLERPKENLPDPTSNATSRGAEPRLPPSPMAVA 229
DB 421 GSRGASGPAGVAGPNDAGRP--EGLMGPPKGLRSP-GNIGPAKEPVP--GLPGID 474
QY 230 GAAGGLALLILGVAGAGAMCWRRRRARPPSSRRPG-----PSGRGSGSLGGG-G 281
DB 475 GRPPG-----IGPAG-----RGPBNIGFPQPKGPTGDPGKNGDKGHAGLAGARG 520
QY 282 GMGP-----REAPRGELTALRG-----GAAPP-----FCPHYEKVSGDYH 321
DB 521 ABPGPGNNGAQGPDPQGV--QGGKGEQGPAGPPGQPLPSPSGPAGVGP 570

RESULT 14
US-11-186-284-31
; Sequence 31, Application US/11186284
; Publication No. US2005026493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamackar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MEMO1-0292RNM
; FILE REFERENCE: MEMO1-0292RNM
; CURRENT APPLICATION NUMBER: US/11/186,284
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FaastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 1366
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-186-284-31

Query Match          7.3%; Score 134.5; DB 7; Length 1366;
Best Local Similarity 25.3%; Pred. No. 0.0033;
Matches 89; Conservative 14; Mismatches 114; Indels 135; Gaps 22;

QY 3 PPHSGPGV--RYGALLILGLVGLVSGLSLEPYVWNSANKRFQAEQGYLYPQIGRLDL 60
DB 321 PGLPBRGILPGVGAAGATGARGLVGEPPAPASKESGKSGAGSAG-----PQ----- 369
QY 61 LCPRARPPGHSSPNYEFYKLYLVGAQGR-----CEAPPAENLLTCDRPDLRLTF 113
DB 370 -----GPPGP-----SGEGRKRPNGAGSAGPPG----- 395
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QY      114  TIKFEYSYPLNLMGHEFRSHNDYUUTATSPQTEBGEESLQGVCLTGMKYLIVG--QSPR 172
Db      396  -----PGLRG-----SFSQR  GLRGADG-----RAGYMGPR 420

QY      173  GGAVERKRVSENMERMDRGAHSLER--GKENTLPGDPTSNATSRGAEGRLPPSPRAYA 229
Db      421  GSRGASGAGVAGVGRPGNDAGRPG--EELGLMGPRGLPSP--GNIGRPAKEXGV---GLPGID 474

QY      230  GAAGGLATLLLCVAAAGACMCRRRRRAKSESNNPG-----PGSFGRGSLGLGGG-G 281
Db      475  GRPGR-----IGRPAQ-----RGEFGNIGFPRPKGRPTGDPGNGGKGAAGLGGARG 520

QY      282  GMGP-----REAPGELGIALRGG-----GAADPR-----PCPHYEKVSGDYGNP 321
Db      521  APGRPGNNGAGQSPRPGQGV--QGSKEGQSPRAGPRPGQGLRGSBSPGAEVNGKP 570

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RESULT 15
US-11-186-284-28
; Sequence 28, Application US/11186284
; Publication No. US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; TITLE OF INVENTION: BURGART, LAWRENCE J.
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MEM01-029P2RM
; CURRENT APPLICATION NUMBER: US/11/186,284
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 1464
; TYPE: PRT
; ORGANISM: Homo Sapiens
; US-11-186-284-28

```

Query Match	7.2%;	Score 133;	DB 7;	Length 1464;
Best Local Similarity	25.8%;	Pred. No. 0.0047;		
Matches	99;	Conservative	19;	Mismatches 128;
				Indels 138;
				Gaps 23

Qy	2	GPSPGPGGVYGAALLLGLVGLVSGLSLEPYVMNSANKRFQAEAGYVLPIQGRDLI	61
Db	848	GPP--GPIG-NVGAAGAKGARG---SAGP-----PGATGFPGAAKRVGP	886
Qy	62	CP--RARPSPGHSSENYEFYKLYLVGAQGRCE-----APPAENLLITCDR	106
Db	887	GPSGAGPGRPGRPAKGE---GGKSPRGEGTGPAPRGPEVGPDPGP	930
Qy	107	PDLDRPTIKQOEVSPNIMGHEFRSHDDYIIATSDGT--REGLESLGGVCL---TR	159
Db	931	-----AGEKSGPPGADGP-----ACAGPTGPGQIGAGCGVGLPGQGRGR	970
Qy	160	GMKVLRLVG-----QSPRGAVPRKRVSEM-----PMEDRGAASLSL--PKENILP	204
Db	971	GFPGI.PGPSGEBQKQGPSGASGERKPPGPMGPGIAGPGESEGRGAPAALESPPRDSGP	1030

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Qy      205  GDFPISNNTSGAGBSELPPSPHPAVAGAAGLALLLLGVAAGGAGMCMRRRAKXSESHP  264
Db      1031  G----AKGDKRETPPAGPPGAPGAPGAP-----VBPAGSG-----DRGET  1069

Qy      265  GP-GSFGRGSLG-GGGGGKMP-----EAPGELIALRG-----GAADPPFCPHYE  312
Db      1070  GPAGPPAGPVGPGVAGKAPGAPGPGGPDGYGTGEGDRIKGRGPGSLGPPGPPGSGPQD  1129

Qy      313  KVSGDYGHPIVTVDDGP--PQSP  334
Db      1130  GPSSG-----ASGPAGPRGRP  1144

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Search completed: December 21, 2005, 14:55:35
Job time : 7.41509 secs

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QY 121 SPNLMGHERSHHDYIIATSDGTREGLESLOGGVCLTRGMKVLRLVQSPRGGAVPKRP 180
DB 121 SPNLMGHERSHHDYIIATSDGTREGLESLOGGVCLTRGMKVLRLVQSPRGGAVPKRP 180
QY 181 VSEMEMERDRGAHSLPEKENTLPGDPTSNATSRGAEGPLPPSPMPAVAGAAGLALLLL 240
DB 181 VSEMEMERDRGAHSLPEKENTLPGDPTSNATSRGAEGPLPPSPMPAVAGAAGLALLLL 240
QY 241 GVAAGAGAMCWRRRRAKPSRHPPGSGFRGSGSLGCGGGMGPBEAPGELGIALRGG 300
DB 241 GVAAGAGAMCWRRRRAKPSRHPPGSGFRGSGSLGCGGGMGPBEAPGELGIALRGG 300
QY 301 GAADPPFCPHYEKVSGDYGHPIYIVODGPPSPNNIYYISVLEMPILHTTOLFPMRSK 360
DB 301 GAADPPFCPHYEKVSGDYGHPIYIVODGPPSPNNIYYISVLEMPILHTTOLFPMRSK 360
QY 361 CSRVTTFEPVYITSTCRMTSFSFTLNPSMOACRAMGEPRIWCFMGRIIGTALF 420
DB 361 CSRVTTFEPVYITSTCRMTSFSFTLNPSMOACRAMGEPRIWCFMGRIIGTALF 420
QY 421 VLVLLILGLRLNMHQTTLRLORASVEAEAGOHGPL 455
DB 421 VLVLLILGLRLNMHQTTLRLORASVEAEAGOHGPL 455

RESULT 2
US-08-635-130A-4
Sequence 4, Application US/08635130A
Patent No. 6696557
GENERAL INFORMATION:
APPLICANT: Caras, Ingrid W
TITLE OF INVENTION: A2-1 Neurotrophic Factor
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 Inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPacIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/635,130A
FILING DATE: 19-Mar-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Phd., Timechy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 340 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-635-130A-4

Query Match 75.1%; Score 1841; DB 2; Length 340;
Best Local Similarity 100.0%; Pred. No. 5, 5e-148;
Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGPPIHSGPGVAVGALLLGLVGLSLPEVYVNSANKRFOAEGGYVLYPOIGDRLLD 60
DB 1 MGPPIHSGPGVAVGALLLGLVGLSLPEVYVNSANKRFOAEGGYVLYPOIGDRLLD 60
QY 61 LCPRARPPGPHSSPNVEFYKLYLVGAQGRCEAPAPNLLITCDRDLDFRTIKFOEY 120
DB 61 LCPRARPPGPHSSPNVEFYKLYLVGAQGRCEAPAPNLLITCDRDLDFRTIKFOEY 120

DB 61 LCPRARPPGPHSSPNVEFYKLYLVGAQGRCEAPAPNLLITCDRDLDFRTIKFOEY 120
QY 121 SPNLMGHERSHHDYIIATSDGTREGLESLOGGVCLTRGMKVLRLVQSPRGGAVPKRP 180
DB 121 SPNLMGHERSHHDYIIATSDGTREGLESLOGGVCLTRGMKVLRLVQSPRGGAVPKRP 180
QY 181 VSEMEMERDRGAHSLPEKENTLPGDPTSNATSRGAEGPLPPSPMPAVAGAAGLALLLL 240
DB 181 VSEMEMERDRGAHSLPEKENTLPGDPTSNATSRGAEGPLPPSPMPAVAGAAGLALLLL 240
QY 241 GVAAGAGAMCWRRRRAKPSRHPPGSGFRGSGSLGCGGGMGPBEAPGELGIALRGG 300
DB 241 GVAAGAGAMCWRRRRAKPSRHPPGSGFRGSGSLGCGGGMGPBEAPGELGIALRGG 300
QY 301 GAADPPFCPHYEKVSGDYGHPIYIVODGPPSPNNIYY 338
DB 301 GAADPPFCPHYEKVSGDYGHPIYIVODGPPSPNNIYY 338

RESULT 3
US-09-949-016-6076
Sequence 6076, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6076
LENGTH: 340
TYPE: PRT
ORGANISM: Human
US-09-949-016-6076

Query Match 75.1%; Score 1841; DB 2; Length 340;
Best Local Similarity 100.0%; Pred. No. 5, 5e-148;
Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGPPIHSGPGVAVGALLLGLVGLSLPEVYVNSANKRFOAEGGYVLYPOIGDRLLD 60
DB 1 MGPPIHSGPGVAVGALLLGLVGLSLPEVYVNSANKRFOAEGGYVLYPOIGDRLLD 60
QY 61 LCPRARPPGPHSSPNVEFYKLYLVGAQGRCEAPAPNLLITCDRDLDFRTIKFOEY 120
DB 61 LCPRARPPGPHSSPNVEFYKLYLVGAQGRCEAPAPNLLITCDRDLDFRTIKFOEY 120
QY 121 SPNLMGHERSHHDYIIATSDGTREGLESLOGGVCLTRGMKVLRLVQSPRGGAVPKRP 180
DB 121 SPNLMGHERSHHDYIIATSDGTREGLESLOGGVCLTRGMKVLRLVQSPRGGAVPKRP 180
QY 181 VSEMEMERDRGAHSLPEKENTLPGDPTSNATSRGAEGPLPPSPMPAVAGAAGLALLLL 240
DB 181 VSEMEMERDRGAHSLPEKENTLPGDPTSNATSRGAEGPLPPSPMPAVAGAAGLALLLL 240
QY 241 GVAAGAGAMCWRRRRAKPSRHPPGSGFRGSGSLGCGGGMGPBEAPGELGIALRGG 300
DB 241 GVAAGAGAMCWRRRRAKPSRHPPGSGFRGSGSLGCGGGMGPBEAPGELGIALRGG 300
QY 301 GAADPPFCPHYEKVSGDYGHPIYIVODGPPSPNNIYY 338
DB 301 GAADPPFCPHYEKVSGDYGHPIYIVODGPPSPNNIYY 338

```

RESULT 4
US-09-949-016-10967
; Sequence 10967, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10967
; LENGTH: 397
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10967

Query Match          75.1%; Score 1841; DB 2; Length 397;
Best Local Similarity 100.0%; Pred. No. 6,8e-148;
Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGPPIHSGPGVAVGALLLGLVGLVSGLSLEPVYNNANKRFOAEGGYLYPQIGDRDL 60
DB 58 MGPPIHSGPGVAVGALLLGLVGLVSGLSLEPVYNNANKRFOAEGGYLYPQIGDRDL 117
QY 61 LCPRARPPGPHSSPNVEFYKLYLVGAQGRCEAPAPMLLTCDRPDLDLFTTKFOEY 120
DB 118 LCPRARPPGPHSSPNVEFYKLYLVGAQGRCEAPAPMLLTCDRPDLDLFTTKFOEY 177
QY 121 SPNLWGEFRSHHDYIITS DGTREGLESLOGVCLTRGMKYLRLVGSGPRGAVPRXP 180
DB 178 SPNLWGEFRSHHDYIITS DGTREGLESLOGVCLTRGMKYLRLVGSGPRGAVPRXP 237
QY 181 VSEMPERDRGAHSLPEKENVLPDPTSNATSRGAEGPLPPSPMPAVAGAAAGLALL 240
DB 238 VSEMPERDRGAHSLPEKENVLPDPTSNATSRGAEGPLPPSPMPAVAGAAAGLALL 297
QY 241 GVAAGGAMCWRRRRAKPSERHPPGSGFRGSLGLGGGGGMPREAREPGLGIALRG 300
DB 298 GVAAGGAMCWRRRRAKPSERHPPGSGFRGSLGLGGGGGMPREAREPGLGIALRG 357
QY 301 GAADPPFCPHYEKVSGDYGHPIYIVODGPPQSPPNITY 338
DB 358 GAADPPFCPHYEKVSGDYGHPIYIVODGPPQSPPNITY 395

RESULT 5
US-09-214-631-3
; Sequence 3, Application US/09214631
; Patent No. 6413730
; GENERAL INFORMATION:
; APPLICANT: Holland, Sacha
; APPLICANT: Mbemalu, Geraldine
; APPLICANT: Pawson, Tony
; TITLE OF INVENTION: OLGOMERIZED RECEPTORS WHICH AFFECT PATHWAYS REGULATED
; BY TRANSMEMBRANE LIGANDS FOR ELK-RELATED RECEPTOR
; FILE REFERENCE: 11757.23USWO
; CURRENT APPLICATION NUMBER: US/09/214,631
; CURRENT FILING DATE: 1999-03-12
; EARLIER APPLICATION NUMBER: PCT/CA97/00473
; EARLIER FILING DATE: 1997-07-04
; EARLIER APPLICATION NUMBER: 60/021,272
; EARLIER FILING DATE: 1996-07-05
; NUMBER OF SEQ ID NOS: 13

```

```

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 340
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-214-631-3

Query Match          75.0%; Score 1837; DB 2; Length 340;
Best Local Similarity 99.7%; Pred. No. 1.2e-147;
Matches 337; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGPPIHSGPGVAVGALLLGLVGLVSGLSLEPVYNNANKRFOAEGGYLYPQIGDRDL 60
DB 1 MGPPIHSGPGVAVGALLLGLVGLVSGLSLEPVYNNANKRFOAEGGYLYPQIGDRDL 60
QY 61 LCPRARPPGPHSSPNVEFYKLYLVGAQGRCEAPAPMLLTCDRPDLDLFTTKFOEY 120
DB 61 LCPRARPPGPHSSPNVEFYKLYLVGAQGRCEAPAPMLLTCDRPDLDLFTTKFOEY 120
QY 121 SPNLWGEFRSHHDYIITS DGTREGLESLOGVCLTRGMKYLRLVGSGPRGAVPRXP 180
DB 121 SPNLWGEFRSHHDYIITS DGTREGLESLOGVCLTRGMKYLRLVGSGPRGAVPRXP 180
QY 181 VSEMPERDRGAHSLPEKENVLPDPTSNATSRGAEGPLPPSPMPAVAGAAAGLALL 240
DB 181 VSEMPERDRGAHSLPEKENVLPDPTSNATSRGAEGPLPPSPMPAVAGAAAGLALL 240
QY 241 GVAAGGAMCWRRRRAKPSERHPPGSGFRGSLGLGGGGGMPREAREPGLGIALRG 300
DB 241 GVAAGGAMCWRRRRAKPSERHPPGSGFRGSLGLGGGGGMPREAREPGLGIALRG 300
QY 301 GAADPPFCPHYEKVSGDYGHPIYIVODGPPQSPPNITY 338
DB 301 GAADPPFCPHYEKVSGDYGHPIYIVODGPPQSPPNITY 338

RESULT 6
US-09-051-994-2
; Sequence 2, Application US/09051994A
; Patent No. 6602683
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: BIOLOGICALLY ACTIVE EPH FAMILY LIGANDS
; FILE REFERENCE: REG-341-PCT-US
; CURRENT APPLICATION NUMBER: US/09/051,994A
; CURRENT FILING DATE: 1998-04-24
; EARLIER APPLICATION NUMBER: PCT/US96/17201
; EARLIER FILING DATE: 1996-10-25
; EARLIER APPLICATION NUMBER: 60/007,015
; EARLIER FILING DATE: 1995-10-25
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 340
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: site
; LOCATION: (166)
; OTHER INFORMATION: Xaa=Arg or Gln
US-09-051-994-2

Query Match          74.9%; Score 1835; DB 2; Length 340;
Best Local Similarity 99.7%; Pred. No. 1.8e-147;
Matches 337; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGPPIHSGPGVAVGALLLGLVGLVSGLSLEPVYNNANKRFOAEGGYLYPQIGDRDL 60
DB 1 MGPPIHSGPGVAVGALLLGLVGLVSGLSLEPVYNNANKRFOAEGGYLYPQIGDRDL 60
QY 61 LCPRARPPGPHSSPNVEFYKLYLVGAQGRCEAPAPMLLTCDRPDLDLFTTKFOEY 120
DB 61 LCPRARPPGPHSSPNVEFYKLYLVGAQGRCEAPAPMLLTCDRPDLDLFTTKFOEY 120

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QY 121 SGNLWGEFRSHHDYIIATSDGTREGLESLOGGVCLTRGMKVLLRVGSPRGGAVPKRP 180
DB 121 SGNLWGEFRSHHDYIIATSDGTREGLESLOGGVCLTRGMKVLLRVGSPRGGAVPKRP 180
QY 181 VSEMMEPRRGAAHSLPEKENVLPDPTSNATSRGAEGPLPPSPMAVGAAGLALLL 240
DB 181 VSEMMEPRRGAAHSLPEKENVLPDPTSNATSRGAEGPLPPSPMAVGAAGLALLL 240
QY 241 GVAGAGAMCWRRRRAKPSRSHPGSGSLGLGGGGMGPRAEPGELIALRGG 300
DB 241 GVAGAGAMCWRRRRAKPSRSHPGSGSLGLGGGGMGPRAEPGELIALRGG 300
QY 301 GAADPPFCPHYKESGDYGHPIYIVODGPPSPPNITY 338
DB 301 GAADPPFCPHYKESGDYGHPIYIVODGPPSPPNITY 338

RESULT 7

US-08-436-044-2
; Sequence 2, Application US/08436044
; Patent No. 5624899
; GENERAL INFORMATION:
; APPLICANT: Bennett, Brian D.
; APPLICANT: Matthews, William
; TITLE OF INVENTION: HTK LIGAND
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,044
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/277722
; FILING DATE: 20-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: 902D3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/925-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 336 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-436-044-2

Query Match 25.7%; Score 628.5; DB 1; Length 336;
Best Local Similarity 41.8%; Pred. No. 3.3e-45;
Matches 137; Conservative 49; Mismatches 129; Indels 13; Gaps 5;

QY 14 GALLLLGVGLVSGLSLEPVYNSANKRQAEQGYVLPQIGDRDLDCPPRAPPGPHSS 73
DB 17 GLAMVLCRTAISRSIVLEETIYNSNSKFLPGQGLVLPQIGDKDIIICPKV---DSKTV 73
QY 74 PNVEFYKLVVGAAGRRCEAPAPNLLTCDRPLDLRFTIKFOEYSNMLWGEFRSH 133
DB 74 GQYEVYKVMVDKQADRCTIKKENTPLNCARPDDVAFITIKFOEFSNMLWGLEFQKK 133

QY 134 DYYIIATSDGTREGLESLOGGVCLTRGMKVLLRVGO--SPRGAVPRKVPSEMPER-DR 190
DB 134 DYYIIATSDGTREGLESLOGGVCLTRGMKVLLRVGO--SPRGAVPRKVPSEMPER-DR 190
QY 191 GAHSLPEKENVLPDPTSNATSRGAEGPLPPSPMAVGAAGLALLLGVAGAGAMC 250
DB 191 GAHSLPEKENVLPDPTSNATSRGAEGPLPPSPMAVGAAGLALLLGVAGAGAMC 250
QY 251 WRRRAKPSRSHHPGSGFGRGSLGLGGGGMGPRAEPGELIALRGGAADPPFCPH 310
DB 251 WRRRAKPSRSHHPGSGFGRGSLGLGGGGMGPRAEPGELIALRGGAADPPFCPH 310
QY 311 YEKVSGDYGHPIYIVODGPPSPPNITY 338
DB 311 YEKVSGDYGHPIYIVODGPPSPPNITY 338

RESULT 8

US-08-436-054-2
; Sequence 2, Application US/08436054
; Patent No. 5864020
; GENERAL INFORMATION:
; APPLICANT: Bennett, Brian D.
; APPLICANT: Matthews, William
; TITLE OF INVENTION: HTK LIGAND
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,054
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/277722
; FILING DATE: 20-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: 902D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/925-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 336 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-436-054-2

Query Match 25.7%; Score 628.5; DB 1; Length 336;
Best Local Similarity 41.8%; Pred. No. 3.3e-45;
Matches 137; Conservative 49; Mismatches 129; Indels 13; Gaps 5;

QY 14 GALLLLGVGLVSGLSLEPVYNSANKRQAEQGYVLPQIGDRDLDCPPRAPPGPHSS 73
DB 17 GLAMVLCRTAISRSIVLEETIYNSNSKFLPGQGLVLPQIGDKDIIICPKV---DSKTV 73
QY 74 PNVEFYKLVVGAAGRRCEAPAPNLLTCDRPLDLRFTIKFOEYSNMLWGEFRSH 133
DB 74 GQYEVYKVMVDKQADRCTIKKENTPLNCARPDDVAFITIKFOEFSNMLWGLEFQKK 133
QY 134 DYYIIATSDGTREGLESLOGGVCLTRGMKVLLRVGO--SPRGAVPRKVPSEMPER-DR 190


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Db      134 DYTIIITSTNGSLGELDNQEGVCTRAMKILMKVGQDASAGSARHNGPTRRPELAGTN 193
Qy      191 GAHSLPEPKENILPGDPTSNATRGAEGLPPSPMAVAGAGGLALLLGVAGAGAMC 250
Db      194 GRSSTTSFVKXPNPGSSTDGNSAGHGNNLLGSEVALFAGIAGGCIIFVIIITLVLL 253
Qy      251 WRRRAKPSBSRHPGSGFRGSGSLGCGGCGMPREARPEGLALRGGAADPPFCRH 310
Db      254 KYRRRRKHSPOHTTLLSTLSTLATPKRGGNN---NGSEPSDVIITPLR---TDSVFCRH 306
Qy      311 YEKVSGDYGHPIYIVODGPPQSPNITY 338
Db      307 YEKVSGDYGHPIYIVODGPPQSPNITY 334

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```

RESULT 9
PCT-US95-08812-2
; Sequence 2, Application PC/TUS9508812
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; TITLE OF INVENTION: HTK LIGAND
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Palin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/08812
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: 902PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELETYPE: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 336 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE:
; PCT-US95-08812-2

```

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Query Match      25.7%; Score 628.5; DB 4; Length 336;
Best Local Similarity 41.8%; Pred. No. 3.3e-45;
Matches 137; Conservative 49; Mismatches 129; Indels 13; Gaps 5;

Qy      14 GALLLLGVLGVGLSLPEPYWNSANKRFOAEGVLYPIQIRLLDLCRRARPPPHSS 73
Db      17 GLLMVLCRTAIISSIVLEPIYWNSSNSKFLPGGLVLYPIQIDKDIICKV--DSKTV 73
Qy      74 PNYEFYKLYLVGAQGRCEAPAPNLLTCDRPPDLRFTIKFOEYSPULMGHFRSHH 133
Db      74 GQVEYKVMVNDQADRCTIKKENTPLNCARPDDVKTIFQGFSPULMGLEFQKK 133
Qy      134 DYTIIITSTNGSLGELDNQEGVCTRAMKILMKVGQDASAGSARHNGPTRRPELAGTN 193
Db      134 DYTIIITSTNGSLGELDNQEGVCTRAMKILMKVGQDASAGSARHNGPTRRPELAGTN 193

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Qy      191 GAHSLPEPKENILPGDPTSNATRGAEGLPPSPMAVAGAGGLALLLGVAGAGAMC 250
Db      194 GRSSTTSFVKXPNPGSSTDGNSAGHGNNLLGSEVALFAGIAGGCIIFVIIITLVLL 253
Qy      251 WRRRAKPSBSRHPGSGFRGSGSLGCGGCGMPREARPEGLALRGGAADPPFCRH 310
Db      254 KYRRRRKHSPOHTTLLSTLSTLATPKRGGNN---NGSEPSDVIITPLR---TDSVFCRH 306
Qy      311 YEKVSGDYGHPIYIVODGPPQSPNITY 338
Db      307 YEKVSGDYGHPIYIVODGPPQSPNITY 334

```

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RESULT 10
US-08-213-403-2
; Sequence 2, Application US/08213403
; Patent No. 5512457
; GENERAL INFORMATION:
; APPLICANT: Lyman, Stewart D.
; APPLICANT: Beckmann, M. Patricia
; APPLICANT: Baum, Peter R.
; APPLICANT: Carpenter, Melissa
; TITLE OF INVENTION: No. 5512457el Cytokine Designated elk Ligand
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple System 7.1
; SOFTWARE: Microsoft Word for Apple, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/213,403
; FILING DATE: 15-MAR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,693
; FILING DATE: 13-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2807-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 346 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-213-403-2

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```

Query Match      25.4%; Score 623; DB 1; Length 346;
Best Local Similarity 39.2%; Pred. No. 1e-44;
Matches 143; Conservative 48; Mismatches 116; Indels 58; Gaps 9;

Qy      8 PGAVRGALLLLGVLGVGL-----SLPEPYWNSANKRFOAEGVLYPIQIRLLD 61
Db      4 PGQRLWLGKVLVMVWVWALCRLATPLAKNLEPVSWSLNRPKLSGKGLVYPKIGDLDT 63
Qy      62 CPRARPGRPSHPNIEFYKLYLVGAQGRCEAPAPNLLTCDRPPDLRFTIKFOEYS 121
Db      64 CRRALGRP-----YHYTLVLRPEQAACSTVLDPNVLVCNRPQEGIRFTIKFOES 118
Qy      122 PNLMGHFRSHHDYIIATSDGTRGSLGQGVCLTRGMKYLRLVGSPPGGAVPRKRV 181
Db      119 PNYMGLEFKHHDYIITSTNGSLGELNREGEVCTRTMKILMKVGQDAPNAVTPEQLTT 178

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QY 182 SEMPERDRGAHSL-PEKENLPDPTSNATSRGAEGPLPPSPMAVAGAAGLA----- 236
DB 179 SRPSKADNTVMATQAGSRGSLDSDGKHETVNOEKSQP-----GASGSGSGDD 231
QY 237 -----LILLGVAAGAGA-----MCMRRRAKPSBSRHPGSGSGSLCL 277
DB 232 GFNSKVALFAAVAGACVIFLLIIFLVLLKLRKRHRKHTQO-----RAAALSL 282
QY 278 -----GGGGMGPRAEPGELGIALRGGAADPPCPHYEKVSGDYGHPIYIVODGPPOSP 333
DB 283 STLASPKGSGGTAGTSPDIIIPLR---TTENNYPHYEKVSGDYGHPIYIVQEMPPOSP 339
QY 334 PNYY 338
DB 340 ANIYY 344
RESULT 11
US-08-458-077-2
Sequence 2, Application US/08458077
Patent No. 5627267
GENERAL INFORMATION:
APPLICANT: Lyman, Stewart D.
APPLICANT: Beckmann, M. Patricia
APPLICANT: Baum, Peter R
APPLICANT: Carpenter, Melissa
TITLE OF INVENTION: No. 5627267el Cytokine Designated elk Ligand
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word for Apple, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,077
FILING DATE: 01-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/213,403
FILING DATE: 15-MAR-1994
APPLICATION NUMBER: US 07/977,693
FILING DATE: 13-NOV-1992
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2807-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 346 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-458-077-2
Query Match 25.4%; Score 623; DB 1; Length 346;
Best Local Similarity 39.2%; Pred. No. 1e-44;
Matches 143; Conservative 48; Mismatches 116; Indels 58; Gaps 9;
QY 8 PGGRVYGALLLGLVLSGL-----SLPPYVWNSANKRFOAGGVLYLPQGLDILL 61
DB 4 PGGRWIGKMLVAVVAVVALCRLATPLAKNLBPVSWSSINPRLPSGKGLVIYPKIGDLDII 63

QY 62 CBRAPPGPHSSPNYEFKLYLVGGAQGRCEAPPAENLLTCRBDLRLFTIKFOYS 121
DB 64 CBRAGARP-----YEVKLYLVREDOAAACSTVLDPVLLVCNBPBORIRFTIKFOEFS 118
QY 122 PVLNGHERSHHDYITITSDOTRGLSLOGVCLTGMKLYLVVGOSPRGAVPRKV 181
DB 119 PVMGLIEFKHHDYITITSNSLGLNREGVCVTRTKIMKVGODPNVATPEQLTT 178
QY 182 SEMPERDRGAHSL-PEKENLPDPTSNATSRGAEGPLPPSPMAVAGAAGLA----- 236
DB 179 SRPSKADNTVMATQAGSRGSLDSDGKHETVNOEKSQP-----GASGSGSGDD 231
QY 237 -----LILLGVAAGAGA-----MCMRRRAKPSBSRHPGSGSGSLCL 277
DB 232 GFNSKVALFAAVAGACVIFLLIIFLVLLKLRKRHRKHTQO-----RAAALSL 282
QY 278 -----GGGGMGPRAEPGELGIALRGGAADPPCPHYEKVSGDYGHPIYIVODGPPOSP 333
DB 283 STLASPKGSGGTAGTSPDIIIPLR---TTENNYPHYEKVSGDYGHPIYIVQEMPPOSP 339
QY 334 PNYY 338
DB 340 ANIYY 344
RESULT 12
US-08-460-741-2
Sequence 2, Application US/08460741
Patent No. 5670625
GENERAL INFORMATION:
APPLICANT: Lyman, Stewart D.
APPLICANT: Beckmann, M. Patricia
APPLICANT: Baum, Peter R
APPLICANT: Carpenter, Melissa
TITLE OF INVENTION: No. 5670625el Cytokine Designated elk Ligand
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word for Apple, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,741
FILING DATE: 02-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/213,403
FILING DATE: 15-MAR-1994
APPLICATION NUMBER: US 07/977,693
FILING DATE: 13-NOV-1992
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2807-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 346 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-460-741-2

Query Match 25.4%; Score 623; DB 1; Length 346;
Best Local Similarity 39.2%; Pred. No. 1e-44;
Matches 143; Conservative 48; Mismatches 116; Indels 58; Gaps 9;

QY 8 PGGVVGLALLGLVLSGL-----SLEPYWNSANKRFOAEGGYLYVPOIGRLDIL 61
DB 4 PGQWLGKMLVAMVWVWALCRLATPLAKNLEPVSWSLNPKFLSGKGLVYPIKIGDLDII 63
QY 62 CRRARPPGHSSNVEFYLYLYVGAQGRCEAPRNILITCDRDLRLRTIKFOES 121
DB 64 CRRARPPGHSSNVEFYLYLYVGAQGRCEAPRNILITCDRDLRLRTIKFOES 118
QY 122 PNLNGHEPSSHHDYIIATSDGTREGLESLOGVCLTRGKYLRLVVGOSPRGAVPRKRV 181
DB 119 PNYMGLFEKQHDYITTSNGSLGLENRGEGVCKRTMKIIMKVGQDPNAVTPBQLTT 178
QY 182 SEMPERDRGAASHLE-PGKENVLPDPTSNATSRGAEGPLPPSPBVAAGAAGLA----- 236
DB 179 SRPSKADNTVMATQAPGSRGSLGSDGKHETVNOEKSFG-----GASGSSGDDP 231
QY 237 -----LILLGVAAGAGA-----MCRRRRAKPSERHPPGSGRGSGL 277
DB 232 GFNSKVALFAAVGACCVIFLLIIFLVLLKLRKRKHRTQO-----RAALSL 282
QY 278 -----GGGGMGPREAPRGELGIALRGGAADPPFCPHYEKVSGDYGHVYIVODGPPSP 333
DB 283 STLSPKGGSGTAGTEPSDIIIFLR--TTENNYCPHYEKVSGDYGHVYIVODGPPSP 339
QY 334 PNIYY 338
DB 340 ANIYY 344

RESULT 13
US-08-747-240-2
Sequence 2, Application US/08747240

PATENT No. 5728613
GENERAL INFORMATION:
APPLICANT: Lyman, Stewart D.
APPLICANT: Beckmann, M. Patricia
APPLICANT: Baum, Peter R.
APPLICANT: Carpenter, Melissa
TITLE OF INVENTION: No. 5728613el Cyclokin Designated elk ligand
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word for Apple, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/747,240
FILING DATE: 12-NOV-1996
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/213,403
FILING DATE: 15-MAR-1994
APPLICATION NUMBER: US 07/977,693
FILING DATE: 13-NOV-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2807-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430

TELEFAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 346 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-747-240-2

Query Match 25.4%; Score 623; DB 1; Length 346;
Best Local Similarity 39.2%; Pred. No. 1e-44;
Matches 143; Conservative 48; Mismatches 116; Indels 58; Gaps 9;

QY 8 PGGVVGLALLGLVLSGL-----SLEPYWNSANKRFOAEGGYLYVPOIGRLDIL 61
DB 4 PGQWLGKMLVAMVWVWALCRLATPLAKNLEPVSWSLNPKFLSGKGLVYPIKIGDLDII 63
QY 62 CRRARPPGHSSNVEFYLYLYVGAQGRCEAPRNILITCDRDLRLRTIKFOES 121
DB 64 CRRARPPGHSSNVEFYLYLYVGAQGRCEAPRNILITCDRDLRLRTIKFOES 118
QY 122 PNLNGHEPSSHHDYIIATSDGTREGLESLOGVCLTRGKYLRLVVGOSPRGAVPRKRV 181
DB 119 PNYMGLFEKQHDYITTSNGSLGLENRGEGVCKRTMKIIMKVGQDPNAVTPBQLTT 178
QY 182 SEMPERDRGAASHLE-PGKENVLPDPTSNATSRGAEGPLPPSPBVAAGAAGLA----- 236
DB 179 SRPSKADNTVMATQAPGSRGSLGSDGKHETVNOEKSFG-----GASGSSGDDP 231
QY 237 -----LILLGVAAGAGA-----MCRRRRAKPSERHPPGSGRGSGL 277
DB 232 GFNSKVALFAAVGACCVIFLLIIFLVLLKLRKRKHRTQO-----RAALSL 282
QY 278 -----GGGGMGPREAPRGELGIALRGGAADPPFCPHYEKVSGDYGHVYIVODGPPSP 333
DB 283 STLSPKGGSGTAGTEPSDIIIFLR--TTENNYCPHYEKVSGDYGHVYIVODGPPSP 339
QY 334 PNIYY 338
DB 340 ANIYY 344

RESULT 14
US-08-299-567-6
Sequence 6, Application US/08299567

PATENT No. 5747033
GENERAL INFORMATION:
APPLICANT: Davis, et al.
TITLE OF INVENTION: METHOD OF ENHANCING THE BIOLOGICAL
TITLE OF INVENTION: ACTIVITY OF BPH FAMILY LIGANDS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Regeneron Pharmaceuticals, Inc.
STREET: 777 Old Saw Mill River Road
CITY: Tarrytown
STATE: New York
COUNTRY: U.S.A.
ZIP: 10591-6707

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/299,567
FILING DATE: 01-SEP-1994
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Kempler, Gail M.
REGISTRATION NUMBER: 32,143
REFERENCE/DOCKET NUMBER: REG 290
TELECOMMUNICATION INFORMATION:
TELEPHONE: 914-345-7400

TELEFAX: 914-345-7721
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 346 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-299-567-6

Query Match 25.4%; Score 623; DB 1; Length 346;
Best Local Similarity 39.2%; Pred. No. 1e-44;
Matches 143; Conservative 48; Mismatches 116; Indels 58; Gaps 9;

QY PGQVRVALLLLGLVLSGL-----SLPEVYWNSSANKRFOAEGGYLVYPOIGRLDLL 61
DB 4 PGQRMIGKRLVAMVWALCRLATPLAKNLEPVSSINPKFSLGKGLVYIPKIGDLIDII 63
QY 62 CPRARPPGHSSPNYEFYKLVVGAQGRRCAPPAENLLITCDRPDLIRFTIKFOEYS 121
DB 64 CPRAEAGRP-----YEYKLVYVRPEQAAACSTVLDPNVLVTCNRPBQETIRFTIKFOEYS 118
QY 122 PNLMGHEFRSHHDYIITSDTRREGLESLOGGVCLTRGKVLRLVGSPPRGAVPRKV 181
DB 119 PNYMGLFQKHHDYIITSTNSGLEENREGVCRTKTKIIMKVGDOPNAVTPBQLTT 178
QY 182 SEMPERDRGAHSLR-PGKENTLPGDPTSNATSRGAEGPLPPSPMPAVAGAAGLA---- 236
DB 179 SRPSKADNTVYKMATQAPGSRGSLGSDGKHETVNOEKSQP-----GAGGSSGDDP 231
QY 237 -----LALLGVAGAGA-----MCMRRRAKPSERSRHPGSGFGRGSLGL 277
DB 232 GFNSKVALLFAAVGAGCVIFLLIIFLVLLKLKRKRKHQTQO-----RAAALSL 282
QY 278 -----GGGGMGRBAEPGSLGIALRGGAADPPFCPHYKVSQDGHPIVYVODGPPSP 333
DB 283 STLASPKGSGTAGTEPSDIIIPLR--TTENNVCPHYEKVSGDYGHPIVYVODGPPSP 339
QY 334 PNITYY 338
DB 340 ANITYY 344

RESULT 15

US-09-039-642B-2
Sequence 2, Application US/09039642B
Patent No. 6540992
GENERAL INFORMATION:
APPLICANT: Lyman, Stewart D.
APPLICANT: Beckmann, M. Patricia
APPLICANT: Baum, Peter R.
APPLICANT: Carpenter, Melissa K.
TITLE OF INVENTION: NOVEL CYTOKINE DESIGNATED ELK LIGAND
FILE REFERENCE: GENENT.67CPDV3
CURRENT APPLICATION NUMBER: US/09/039,642B
CURRENT FILING DATE: 1998-03-16
PRIORITY APPLICATION NUMBER: 08/213,403
PRIORITY FILING DATE: 1994-03-15
PRIORITY APPLICATION NUMBER: 07/977,693
PRIORITY FILING DATE: 1992-11-13
PRIORITY APPLICATION NUMBER: 08/747,240
PRIORITY FILING DATE: 1996-10-12
PRIORITY APPLICATION NUMBER: 08/460,741
PRIORITY FILING DATE: 1995-06-02
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 346
TYPE: PRT
ORGANISM: Homo sapiens
US-09-039-642B-2

Query Match 25.4%; Score 623; DB 2; Length 346;

Best Local Similarity 39.2%; Pred. No. 1e-44;
Matches 143; Conservative 48; Mismatches 116; Indels 58; Gaps 9;

QY 8 PGQVRVALLLLGLVLSGL-----SLPEVYWNSSANKRFOAEGGYLVYPOIGRLDLL 61
DB 4 PGQRMIGKRLVAMVWALCRLATPLAKNLEPVSSINPKFSLGKGLVYIPKIGDLIDII 63
QY 62 CPRARPPGHSSPNYEFYKLVVGAQGRRCAPPAENLLITCDRPDLIRFTIKFOEYS 121
DB 64 CPRAEAGRP-----YEYKLVYVRPEQAAACSTVLDPNVLVTCNRPBQETIRFTIKFOEYS 118
QY 122 PNLMGHEFRSHHDYIITSDTRREGLESLOGGVCLTRGKVLRLVGSPPRGAVPRKV 181
DB 119 PNYMGLFQKHHDYIITSTNSGLEENREGVCRTKTKIIMKVGDOPNAVTPBQLTT 178
QY 182 SEMPERDRGAHSLR-PGKENTLPGDPTSNATSRGAEGPLPPSPMPAVAGAAGLA---- 236
DB 179 SRPSKADNTVYKMATQAPGSRGSLGSDGKHETVNOEKSQP-----GAGGSSGDDP 231
QY 237 -----LALLGVAGAGA-----MCMRRRAKPSERSRHPGSGFGRGSLGL 277
DB 232 GFNSKVALLFAAVGAGCVIFLLIIFLVLLKLKRKRKHQTQO-----RAAALSL 282
QY 278 -----GGGGMGRBAEPGSLGIALRGGAADPPFCPHYKVSQDGHPIVYVODGPPSP 333
DB 283 STLASPKGSGTAGTEPSDIIIPLR--TTENNVCPHYEKVSGDYGHPIVYVODGPPSP 339
QY 334 PNITYY 338
DB 340 ANITYY 344

Search completed: December 21, 2005, 14:37.38
Job time : 38.2013 secs

GenCore version 5.1.6
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OW protein - protein search, using sw model

Run on: December 21, 2005, 14:30:39 ; Search time 128.201 Seconds
(without alignments)
1482.921 Million cell updates/sec

Title: US-10-021-121-2

Perfect score: 2450

Sequence: 1 MGPPIHSGPGVGVGALLILG.....TTLLRQASVEAAGHGPL 455

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications AA Main:*
1: /cgn2_6/prodata/1/pubppa/US07_PUBCOMB.pep:*
2: /cgn2_6/prodata/1/pubppa/US08_PUBCOMB.pep:*
3: /cgn2_6/prodata/1/pubppa/US09_PUBCOMB.pep:*
4: /cgn2_6/prodata/1/pubppa/US10A_PUBCOMB.pep:*
5: /cgn2_6/prodata/1/pubppa/US10B_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2450	100.0	455	4	US-10-021-121-2
2	1841	75.1	340	4	US-10-021-121-4
3	1841	75.1	340	5	US-10-723-860-4256
4	1841	75.1	340	5	US-10-698-907-16
5	1837	75.0	340	4	US-10-138-787-3
6	1835	74.9	340	4	US-10-417-924A-2
7	1771	72.3	340	5	US-10-698-907-8
8	1550	63.3	285	4	US-10-08-765A-2695
9	628.5	25.7	336	5	US-10-698-907-7
10	623	25.4	346	4	US-10-021-121-9
11	623	25.4	346	4	US-10-356-289-2
12	623	25.4	346	4	US-10-712-124-60
13	623	25.4	346	4	US-10-789-378-30
14	623	25.4	346	5	US-10-698-907-14
15	620.5	25.3	333	3	US-09-754-105-2
16	620.5	25.3	333	3	US-09-878-339-2
17	620.5	25.3	333	4	US-10-021-121-10
18	620.5	25.3	333	4	US-10-331-496A-63
19	620.5	25.3	333	5	US-10-696-639-62
20	620.5	25.3	333	5	US-10-696-639-15
21	620.5	25.3	333	5	US-10-800-350-396
22	620.5	25.3	333	5	US-10-800-077-396
23	613.5	25.0	333	4	US-10-138-787-4
24	604.5	24.7	345	5	US-10-698-907-6
25	599.5	24.5	345	4	US-10-138-787-5
26	489	20.0	89	3	US-09-862-179A-17
27	489	20.0	89	4	US-10-138-787-13

28	451.5	18.4	459	5	US-10-800-350-390	Sequence 390, App
29	451.5	18.4	459	5	US-10-800-077-390	Sequence 390, App
30	447	18.2	429	5	US-10-698-907-20	Sequence 20, App
31	443	18.1	226	5	US-10-698-907-21	Sequence 21, App
32	442	18.0	233	5	US-10-800-350-388	Sequence 388, App
33	442	18.0	233	5	US-10-800-077-388	Sequence 388, App
34	284.5	11.6	92	3	US-09-864-761-48262	Sequence 48262, A
35	196.5	8.0	136	3	US-09-864-761-48257	Sequence 48257, A
36	193.5	7.9	106	3	US-09-925-297-639	Sequence 639, App
37	192	7.8	82	3	US-09-862-179A-15	Sequence 15, App
38	182	7.8	82	4	US-10-138-787-11	Sequence 11, App
39	192	7.8	652	6	US-11-097-143-2635	Sequence 2635, App
40	192	7.8	652	6	US-11-097-143-23436	Sequence 23436, A
41	191.5	7.8	82	3	US-09-862-179A-16	Sequence 16, App
42	191.5	7.8	82	4	US-10-138-787-12	Sequence 12, App
43	179	7.3	238	3	US-09-904-954-2	Sequence 2, App
44	179	7.3	238	3	US-09-733-756-2	Sequence 2, App
45	179	7.3	238	4	US-10-241-220-72	Sequence 72, App

ALIGNMENTS

RESULT 1
US-10-021-121-2

Sequence 2, Application US/10021121

Publication No. US2002014244A1

GENERAL INFORMATION:

APPLICANT: Caras, Ingrid W

TITLE OF INVENTION: A2-1 Neurotrophic Factor

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatlin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/021,121

FILING DATE: 06-Dec-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/635,130

FILING DATE: 19-Mar-1996

ATTORNEY/AGENT INFORMATION:

NAME: Torchia, PhD., Timothy E.

REGISTRATION NUMBER: 36,700

REFERENCE/DOCKET NUMBER: P1001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-8674

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 455 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-10-021-121-2

Query Match 100.0%; Score 2450; DB 4; Length 455;
Best Local Similarity 100.0%; Pred. No. 1.6e-179;
Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGPPIHSGPGVGVGALLILGVGSLSEPVYNNANKRFOAEGGYLYPOIGRDL 60
DB 1 MGPPIHSGPGVGVGALLILGVGSLSEPVYNNANKRFOAEGGYLYPOIGRDL 60

QY 61 LCPRRARPPGPHSSPNVEFYKLYLVGGAQGRCEAPAPVLLTCDRPDLDLFTTKFOEY 120
DB 61 LCPRRARPPGPHSSPNVEFYKLYLVGGAQGRCEAPAPVLLTCDRPDLDLFTTKFOEY 120
QY 121 SPNLWGHFRSHHDYIITATSDGTREGLESLOGVCLTRGMKYLVRVGSPPGGAAPRRP 180
DB 121 SPNLWGHFRSHHDYIITATSDGTREGLESLOGVCLTRGMKYLVRVGSPPGGAAPRRP 180
QY 181 VSEMPMERDRGAHSLPECKENLPDPTSNATSRGAEGPLPPSPMPAVAGAAGLALL 240
DB 181 VSEMPMERDRGAHSLPECKENLPDPTSNATSRGAEGPLPPSPMPAVAGAAGLALL 240
QY 241 GYAAGAGAMCWMRRRAKPSRRHPGSGFRGSGSLGGGGGMPREABPGLGIALRG 300
DB 241 GYAAGAGAMCWMRRRAKPSRRHPGSGFRGSGSLGGGGGMPREABPGLGIALRG 300
QY 301 GAADPPFCPHYEKVSGDYGHPIYIVODGPPQSPNNIYYISVLEMPILHTTOLFFMRK 360
DB 301 GAADPPFCPHYEKVSGDYGHPIYIVODGPPQSPNNIYYISVLEMPILHTTOLFFMRK 360
QY 361 CSRVTTFLEPVQYITTSCTMTSFSFTTLNPSMQACRAQMGFEFRIRWCFMGDRILGTALF 420
DB 361 CSRVTTFLEPVQYITTSCTMTSFSFTTLNPSMQACRAQMGFEFRIRWCFMGDRILGTALF 420
QY 421 VLVLLILGLRLNHQTTLLRQRASVEAEGQHGPL 455
DB 421 VLVLLILGLRLNHQTTLLRQRASVEAEGQHGPL 455

RESULT 2
US-10-021-121-4

Sequence 4, Application US/10021121
Publication No. US20020142444A1
GENERAL INFORMATION:

APPLICANT: Caras, Ingrid W
TITLE OF INVENTION: A2-1 Neurotrophic Factor
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/021,121
FILING DATE: 06-Dec-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/635,130
FILING DATE: 19-Mar-1996
ATTORNEY/AGENT INFORMATION:

NAME: Torchia, PhD., Timothy B.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-9881
TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
LENGTH: 340 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-021-121-4

Query Match 75.1%; Score 1841; DB 4; Length 340;
Best Local Similarity 100.0%; Pred. No. 6.4e-133;

Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MCPPHSPPGCVVAGALLLGLVGLSVGLSEFVYNNANKRQABGGYLYPQIGRDL 60
DB 1 MCPPHSPPGCVVAGALLLGLVGLSVGLSEFVYNNANKRQABGGYLYPQIGRDL 60
QY 61 LCPRRARPPGPHSSPNVEFYKLYLVGGAQGRCEAPAPVLLTCDRPDLDLFTTKFOEY 120
DB 61 LCPRRARPPGPHSSPNVEFYKLYLVGGAQGRCEAPAPVLLTCDRPDLDLFTTKFOEY 120
QY 121 SPNLWGHFRSHHDYIITATSDGTREGLESLOGVCLTRGMKYLVRVGSPPGGAAPRRP 180
DB 121 SPNLWGHFRSHHDYIITATSDGTREGLESLOGVCLTRGMKYLVRVGSPPGGAAPRRP 180
QY 181 VSEMPMERDRGAHSLPECKENLPDPTSNATSRGAEGPLPPSPMPAVAGAAGLALL 240
DB 181 VSEMPMERDRGAHSLPECKENLPDPTSNATSRGAEGPLPPSPMPAVAGAAGLALL 240
QY 241 GYAAGAGAMCWMRRRAKPSRRHPGSGFRGSGSLGGGGGMPREABPGLGIALRG 300
DB 241 GYAAGAGAMCWMRRRAKPSRRHPGSGFRGSGSLGGGGGMPREABPGLGIALRG 300
QY 301 GAADPPFCPHYEKVSGDYGHPIYIVODGPPQSPNNIYY 338
DB 301 GAADPPFCPHYEKVSGDYGHPIYIVODGPPQSPNNIYY 338

RESULT 3
US-10-723-860-4256

Sequence 4256, Application US/10723860
Publication No. US20040253606A1
GENERAL INFORMATION:

APPLICANT: Aziz, Natasha
APPLICANT: Ginsburg, Wendy W.
APPLICANT: Zlotnick, Albert
TITLE OF INVENTION: Methods for Diagnosis of Soft Tissue Sarcoma, Compositions &
TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators &
FILE REFERENCE: 05882, 0193, NPUS01
CURRENT FILING DATE: 2003-11-26
PRIORITY FILING DATE: 2003-11-26
PRIOR APPLICATION NUMBER: 60/429, 739
NUMBER OF SEQ ID NOS: 8393
SOFTWARE: PatentIn version 3.2
SEQ ID NO 4256
LENGTH: 340
TYPE: PRT
ORGANISM: Homo sapiens
US-10-723-860-4256

Query Match 75.1%; Score 1841; DB 5; Length 340;
Best Local Similarity 100.0%; Pred. No. 6.4e-133;

Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MCPPHSPPGCVVAGALLLGLVGLSVGLSEFVYNNANKRQABGGYLYPQIGRDL 60
DB 1 MCPPHSPPGCVVAGALLLGLVGLSVGLSEFVYNNANKRQABGGYLYPQIGRDL 60
QY 61 LCPRRARPPGPHSSPNVEFYKLYLVGGAQGRCEAPAPVLLTCDRPDLDLFTTKFOEY 120
DB 61 LCPRRARPPGPHSSPNVEFYKLYLVGGAQGRCEAPAPVLLTCDRPDLDLFTTKFOEY 120
QY 121 SPNLWGHFRSHHDYIITATSDGTREGLESLOGVCLTRGMKYLVRVGSPPGGAAPRRP 180
DB 121 SPNLWGHFRSHHDYIITATSDGTREGLESLOGVCLTRGMKYLVRVGSPPGGAAPRRP 180
QY 181 VSEMPMERDRGAHSLPECKENLPDPTSNATSRGAEGPLPPSPMPAVAGAAGLALL 240
DB 181 VSEMPMERDRGAHSLPECKENLPDPTSNATSRGAEGPLPPSPMPAVAGAAGLALL 240
QY 241 GYAAGAGAMCWMRRRAKPSRRHPGSGFRGSGSLGGGGGMPREABPGLGIALRG 300
DB 241 GYAAGAGAMCWMRRRAKPSRRHPGSGFRGSGSLGGGGGMPREABPGLGIALRG 300

Qy 301 GAADPPFCPHYKESGDIYGVYIVODGPPQSPNNITY 338
Db 301 GAADPPFCPHYKESGDIYGVYIVODGPPQSPNNITY 338

RESULT 4
US-10-698-907-16
; Sequence 16, Application US/10698907
; Publication No. US20050049194A1
; GENERAL INFORMATION:
; APPLICANT: Filsen, Jonas
; APPLICANT: Holmberg, Johan
; TITLE OF INVENTION: Use of Ephrins and Related Molecules to Regulate Cellular
; FILE REFERENCE: 21882-529 UTIL
; CURRENT APPLICATION NUMBER: US/10/698,907
; CURRENT FILING DATE: 2003-10-31
; PRIOR APPLICATION NUMBER: US 60/460,488
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: US 10/291,290
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: US 60/393,272
; PRIOR FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US 60/345,206
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 16
; LENGTH: 340
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-698-907-16

Query Match 75.1%; Score 1841; DB 5; Length 340;
Best Local Similarity 100.0%; Pred. No. 6,4e-133;
Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGPPIHSGPGVVRGALLLGLVGLVGLSLLEPYMNSANKRFOAEGGYLYPQIGRLDL 60
Db 1 MGPPIHSGPGVVRGALLLGLVGLVGLSLLEPYMNSANKRFOAEGGYLYPQIGRLDL 60
Qy 61 LCPRARPPGPHSSPNVEFYKLYLVGAQGRCEAPAPNLLTCDRPPDLRLFTIKFOXY 120
Db 61 LCPRARPPGPHSSPNVEFYKLYLVGAQGRCEAPAPNLLTCDRPPDLRLFTIKFOXY 120
Qy 121 SPNLWGEFRSHHDYIIATSDGTREGLESLOGVCLTRGMKVLTVGQSPRGAVPRKP 180
Db 121 SPNLWGEFRSHHDYIIATSDGTREGLESLOGVCLTRGMKVLTVGQSPRGAVPRKP 180
Qy 181 VSEMPERDRGAHSLPEKENVLPDPTSNATSRGAEGLPPSPMVAVGAAGLALLL 240
Db 181 VSEMPERDRGAHSLPEKENVLPDPTSNATSRGAEGLPPSPMVAVGAAGLALLL 240
Qy 241 GVAAGAGAMCWMRRRAKPSRHPGSGFGRGSLGLGGGGMGPRAEPGELGIALRG 300
Db 241 GVAAGAGAMCWMRRRAKPSRHPGSGFGRGSLGLGGGGMGPRAEPGELGIALRG 300
Qy 301 GAADPPFCPHYKESGDIYGVYIVODGPPQSPNNITY 338
Db 301 GAADPPFCPHYKESGDIYGVYIVODGPPQSPNNITY 338

RESULT 5
US-10-138-787-3
; Sequence 3, Application US/10138787
; Publication No. US20020172984A1
; GENERAL INFORMATION:
; APPLICANT: Holland, Sacha
; APPLICANT: Mbamalu, Geraldine
; APPLICANT: Rawson, Tony
; TITLE OF INVENTION: OLIGOMERIZED RECEPTORS WHICH AFFECT PATHWAYS REGULATED
; BY TRANSMEMBRANE LIGANDS FOR ELK-RELATED RECEPTOR

; TITLE OF INVENTION: TYROSINE KINASES
; FILE REFERENCE: 11757.23USMO
; CURRENT APPLICATION NUMBER: US/10/138,787
; CURRENT FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: US/09/214,631
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: PCT/CA97/00473
; PRIOR FILING DATE: 1997-07-04
; PRIOR APPLICATION NUMBER: 60/021,272
; PRIOR FILING DATE: 1996-07-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 3
; LENGTH: 340
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-138-787-3

Query Match 75.0%; Score 1837; DB 4; Length 340;
Best Local Similarity 99.7%; Pred. No. 1.3e-132;
Matches 337; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGPPIHSGPGVVRGALLLGLVGLVGLSLLEPYMNSANKRFOAEGGYLYPQIGRLDL 60
Db 1 MGPPIHSGPGVVRGALLLGLVGLVGLSLLEPYMNSANKRFOAEGGYLYPQIGRLDL 60
Qy 61 LCPRARPPGPHSSPNVEFYKLYLVGAQGRCEAPAPNLLTCDRPPDLRLFTIKFOXY 120
Db 61 LCPRARPPGPHSSPNVEFYKLYLVGAQGRCEAPAPNLLTCDRPPDLRLFTIKFOXY 120
Qy 121 SPNLWGEFRSHHDYIIATSDGTREGLESLOGVCLTRGMKVLTVGQSPRGAVPRKP 180
Db 121 SPNLWGEFRSHHDYIIATSDGTREGLESLOGVCLTRGMKVLTVGQSPRGAVPRKP 180
Qy 181 VSEMPERDRGAHSLPEKENVLPDPTSNATSRGAEGLPPSPMVAVGAAGLALLL 240
Db 181 VSEMPERDRGAHSLPEKENVLPDPTSNATSRGAEGLPPSPMVAVGAAGLALLL 240
Qy 241 GVAAGAGAMCWMRRRAKPSRHPGSGFGRGSLGLGGGGMGPRAEPGELGIALRG 300
Db 241 GVAAGAGAMCWMRRRAKPSRHPGSGFGRGSLGLGGGGMGPRAEPGELGIALRG 300
Qy 301 GAADPPFCPHYKESGDIYGVYIVODGPPQSPNNITY 338
Db 301 GAADPPFCPHYKESGDIYGVYIVODGPPQSPNNITY 338

RESULT 6
US-10-417-924A-2
; Sequence 2, Application US/10417924A
; Publication No. US20030215918A1
; GENERAL INFORMATION:
; APPLICANT: Samuel David, et al.
; TITLE OF INVENTION: BIOLOGICALLY ACTIVE EPH FAMILY LIGANDS
; FILE REFERENCE: REG-3412
; CURRENT APPLICATION NUMBER: US/10/417,924A
; CURRENT FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: 09/051,994
; PRIOR FILING DATE: 1998-04-24
; PRIOR APPLICATION NUMBER: PCT/US96/17201
; PRIOR FILING DATE: 1996-10-25
; PRIOR APPLICATION NUMBER: 60/007,015
; PRIOR FILING DATE: 1995-10-25
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 340
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: Misc. feature
; LOCATION: (166)
; OTHER INFORMATION: Xaa = unknown or other

US-10-417-924A-2

Query Match 74.9%; Score 1835; DB 4; Length 340;
Best Local Similarity 99.7%; Pred. No. 1.8e-132;
Matches 337; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGPBHGPGGVAVGALLLVGLVSGLSLEPYMNSANKRFOAEGGYLYPIQGRDL 60
DB 1 MGPBHGPGGVAVGALLLVGLVSGLSLEPYMNSANKRFOAEGGYLYPIQGRDL 60
QY 61 LCPBAPPGHSSPNTEFYKLYVGAQGRCEAPAPNLLTCDRDLRTIKFOEY 120
DB 61 LCPBAPPGHSSPNTEFYKLYVGAQGRCEAPAPNLLTCDRDLRTIKFOEY 120
QY 121 SPULMGHEFRSHDYYIATS DTRGLESLOGVCILTRGMKYLVRVQSPRGAVPRKP 180
DB 121 SPULMGHEFRSHDYYIATS DTRGLESLOGVCILTRGMKYLVRVQSPRGAVPRKP 180
QY 181 VSEMERDRGAHSLPEKKNLPDPTSNATSRGAEGLPPSPMAVAGAGLALL 240
DB 181 VSEMERDRGAHSLPEKKNLPDPTSNATSRGAEGLPPSPMAVAGAGLALL 240
QY 241 GVAAGAGAMCWRRRRAKPSRRHPGSGFGRGSLGLGGGGMGPRAEPGELG 300
DB 241 GVAAGAGAMCWRRRRAKPSRRHPGSGFGRGSLGLGGGGMGPRAEPGELG 300
QY 301 GAADPPFCPHYEKVSGDYGHPIYIVODGPPQSPNNIY 338
DB 301 GAADPPFCPHYEKVSGDYGHPIYIVODGPPQSPNNIY 338

RESULT 7
US-10-698-907-8
; Sequence 8, Application US/10698907
; Publication No. US20050049194A1

; GENERAL INFORMATION:
; APPLICANT: Friisen, Jonas
; APPLICANT: Holmberg, Johan
; TITLE OF INVENTION: Use of Ephrins and Related Molecules to Regulate Cellular
; FILE REFERENCE: 21882-529 UTIL.
; CURRENT APPLICATION NUMBER: US/10/698, 907
; CURRENT FILING DATE: 2003-10-31
; PRIOR APPLICATION NUMBER: US 60/460,488
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: US 10/291,290
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: US 60/393,272
; PRIOR FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US 60/345,206
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 8
; LENGTH: 340
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-698-907-8

Query Match 72.3%; Score 1771; DB 5; Length 340;
Best Local Similarity 95.6%; Pred. No. 1.5e-127;
Matches 323; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 MGPBHGPGGVAVGALLLVGLVSGLSLEPYMNSANKRFOAEGGYLYPIQGRDL 60
DB 1 MGPBHGPGGVAVGALLLVGLVSGLSLEPYMNSANKRFOAEGGYLYPIQGRDL 60
QY 61 LCPBAPPGHSSPNTEFYKLYVGAQGRCEAPAPNLLTCDRDLRTIKFOEY 120
DB 61 LCPBAPPGHSSPNTEFYKLYVGAQGRCEAPAPNLLTCDRDLRTIKFOEY 120
QY 121 SPULMGHEFRSHDYYIATS DTRGLESLOGVCILTRGMKYLVRVQSPRGAVPRKP 180
DB 121 SPULMGHEFRSHDYYIATS DTRGLESLOGVCILTRGMKYLVRVQSPRGAVPRKP 180

DB 121 SPULMGHEFRSHDYYIATS DTRGLESLOGVCILTRGMKYLVRVQSPRGAVPRKP 180
QY 181 VSEMERDRGAHSLPEKKNLPDPTSNATSRGAEGLPPSPMAVAGAGLALL 240
DB 181 VSEMERDRGAHSLPEKKNLPDPTSNATSRGAEGLPPSPMAVAGAGLALL 240
QY 241 GVAAGAGAMCWRRRRAKPSRRHPGSGFGRGSLGLGGGGMGPRAEPGELG 300
DB 241 GVAAGAGAMCWRRRRAKPSRRHPGSGFGRGSLGLGGGGMGPRAEPGELG 300
QY 301 GAADPPFCPHYEKVSGDYGHPIYIVODGPPQSPNNIY 338
DB 301 GAADPPFCPHYEKVSGDYGHPIYIVODGPPQSPNNIY 338

RESULT 8
US-10-408-765A-2695
; Sequence 2695, Application US/10408765A
; Publication No. US20040101874A1

; GENERAL INFORMATION:
; APPLICANT: Ghost, Soumitra S.
; APPLICANT: Fahy, Bojin D.
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088, 465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2695
; LENGTH: 285
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-2695

Query Match 63.3%; Score 1550; DB 4; Length 285;
Best Local Similarity 100.0%; Pred. No. 1.1e-110;
Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 DRDLDCPRARPPGHSSPNTEFYKLYVGAQGRCEAPAPNLLTCDRDLRTIK 115
DB 1 DRDLDCPRARPPGHSSPNTEFYKLYVGAQGRCEAPAPNLLTCDRDLRTIK 60
QY 116 KQEYSPNLMGHEFRSHDYYIATS DTRGLESLOGVCILTRGMKYLVRVQSPRG 175
DB 116 KQEYSPNLMGHEFRSHDYYIATS DTRGLESLOGVCILTRGMKYLVRVQSPRG 120
QY 176 VPRKPVSEMERDRGAHSLPEKKNLPDPTSNATSRGAEGLPPSPMAVAGAGL 235
DB 176 VPRKPVSEMERDRGAHSLPEKKNLPDPTSNATSRGAEGLPPSPMAVAGAGL 180
QY 236 ALLLVGAVAGAMCWRRRRAKPSRRHPGSGFGRGSLGLGGGGMGPRAEPGELG 295
DB 181 ALLLVGAVAGAMCWRRRRAKPSRRHPGSGFGRGSLGLGGGGMGPRAEPGELG 240
QY 296 ALRGGAADPPFCPHYEKVSGDYGHPIYIVODGPPQSPNNIY 338
DB 241 ALRGGAADPPFCPHYEKVSGDYGHPIYIVODGPPQSPNNIY 283

RESULT 9
US-10-698-907-7
; Sequence 7, Application US/10698907
; Publication No. US20050049194A1
; GENERAL INFORMATION:
; APPLICANT: Friisen, Jonas
; APPLICANT: Holmberg, Johan
; TITLE OF INVENTION: Use of Ephrins and Related Molecules to Regulate Cellular


```

1 TITLE OF INVENTION: Proliferation
2
3 FILE REFERENCE: 21882-529 UTIL
4
5 CURRENT APPLICATION NUMBER: US/10/698,907
6
7 CURRENT FILING DATE: 2003-10-31
8
9 PRIOR APPLICATION NUMBER: US 60/460,488
10
11 PRIOR FILING DATE: 2003-04-03
12
13 PRIOR APPLICATION NUMBER: US 10/291,290
14
15 PRIOR FILING DATE: 2002-11-08
16
17 PRIOR APPLICATION NUMBER: US 60/393,272
18
19 PRIOR FILING DATE: 2002-07-02
20
21 PRIOR APPLICATION NUMBER: US 60/345,206
22
23 PRIOR FILING DATE: 2001-11-09
24
25 NUMBER OF SEQ ID NOS: 25
26
27 SOFTWARE: PatentIn version 3.2
28
29 SEQ ID NO 7
30
31 LENGTH: 336
32
33 TYPE: prt
34
35 ORGANISM: Mus musculus
36
37 US-10-698-907-7

```

[illegible]

RESULT 10
 US-10-021-121-9
 ? Sequence 9, Application US/10021121
 ? Publication No. US20020142444A1
 ? GENERAL INFORMATION:
 ? APPLICANT: Carae, Ingrid W
 ? TITLE OF INVENTION: A2-1 Neurotrophic Factor
 ? NUMBER OF SEQUENCES: 10
 ? CORRESPONDENCE ADDRESS:
 ? ADDRESSEE: Genentech, Inc.
 ? STREET: 1 DNA Way
 ? CITY: South San Francisco
 ? STATE: California
 ? COUNTRY: USA
 ? ZIP: 94080
 ? COMPUTER READABLE FORM:
 ? MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 ? COMPUTER: IBM PC compatible
 ? OPERATING SYSTEM: PC-DOS/MS-DOS
 ? SOFTWARE: Winpacin (Genentech)
 ? CURRENT APPLICATION DATA:
 ? APPLICATION NUMBER: US/10/021, 121
 ? FILING DATE: 06-Dec-2001
 ? CLASSIFICATION: <Unknown>

```

? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US/08/635,130
? FILING DATE: 19-Mar-1996
? ATTORNEY/AGENT INFORMATION:
? NAME: Torchia, Pnd., Timothy E.
? REGISTRATION NUMBER: 36,700
? REFERENCE/DOCKET NUMBER: P1001
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 650/225-8674
? TELEFAX: 650/952-9881
? INFORMATION FOR SEQ ID NO: 9:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 346 amino acids
? TYPE: Amino Acid
? TOPOLOGY: Linear
? SEQUENCE DESCRIPTION: SEQ ID NO: 9:
? US-10-021-121-9

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	Query Match	25.4%; Score 623; DB 4; Length 346;
	Best Local Similarity	39.2%; Pred. No. 2e-39;
	Matches 143; Conservative 48; Mismatches 116; Indels 58; Gaps 9;	
Oy	8 PGYVRGALLILGLVLSGI-----SLEPYWNSANKRFQAEGGVYLTPQIGDRIDL 61	
Dd	4 PGGWMLCKMVLAMVMVMAICRLATPLAQLNLEVSWSINPKFLSGKGVLYIPKIDGDLDII 63	
Oy	62 CPRARPPGPHSSPVYEFEFKYLVVGAGQRREAPPAENLLTCORPDLRFTIKFQEYS 121	
Dd	64 CPRBAQGRP-----YEEYKLYLVAPEQAACSTYLDENVLTCCRPEQEIREFTIKFQEF 118	
Oy	122 PNLMGHESFRSHDDYYIATS DGTREGLESLOGVCLTRGMKVLRVGSQSPRGCAVPRAKV 181	
Dd	119 PNMYGLEPKKHHDYYISTNGSLGLEGNREGVCRTTRMKIIIMKWQDPAVALTPEQLTT 178	
Oy	182 SEMMEDRCGAASHLE-PGENLEPGDPTSNATSRSGACGPLRPSEMPAVAGAAGLA---- 236	
Dd	179 SRPSKEADNTVKATQAPGSRGSLGSDDGKHETYNQEEKSGP-----GASGGSSDDPD 231	
Oy	237 -----LLLLGVAGAGA-----MCWRRRAPXPSERSHPGSGFGSGSLG 277	
Dd	232 GFPMASKALPAAVGACVIFLLIIIFLTVLLIKLRKHKRHKTQQ-----RAALLSL 282	
Oy	278 ----GGGGGCGPREABEPDELGIALRGGAADPFPCPHYEKVSGDYGHPIYITVDGPQPSP 333	
Dd	283 STLASPKGSGSTAGTEPSDIITPLR---TTENNYPCHYEKVS GDYGHPIYIVQEMPPQSP 339	
Oy	334 PNITY 338	
Dd	340 ANITY 344	

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RESULT 11
; US-10-356-289-2
; Sequence 2, Application US/103565289
; Publication No. US20040022767A1
; GENERAL INFORMATION:
; APPLICANT: Lyman, Stewart D.
; APPLICANT: Beckmann, M. Patricia
; APPLICANT: Baum, Peter R.
; APPLICANT: Carpenter, Melissa K.
; TITLE OF INVENTION: NOVEL CYTOKINE DESIGNATED ELK LIGAND
; FILE REFERENCE: GENENT.67CPD3
; CURRENT APPLICATION NUMBER: US/10/356, 289
; CURRENT FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: US/09/039, 642B
; PRIOR FILING DATE: 1998-03-16
; PRIOR APPLICATION NUMBER: 08/213, 403
; PRIOR FILING DATE: 1994-03-15
; PRIOR APPLICATION NUMBER: 07/977, 693
; PRIOR FILING DATE: 1992-11-13
; PRIOR APPLICATION NUMBER: 08/747, 240
; PRIOR FILING DATE: 1996-10-12
; PRIOR APPLICATION NUMBER: 08/460, 741

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PRIOR FILING DATE: 1995-06-02
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 346
TYPE: PRT
ORGANISM: Homo sapiens
US-10-356-289-2

Query Match 25.4%; Score 623; DB 4; Length 346;
Best Local Similarity 39.2%; Pred. No. 2e-39;
Matches 143; Conservative 48; Mismatches 116; Indels 58; Gaps 9;

QY 8 PGQVAVGALLLLGVGLVSGL-----SLEPYWNSANKRFOAEGGYVLYPOIGDRDL 61
DB 4 PGQWVGKVLVAVVWVALCRLATPLAKNLEPVSWSSLNPKFLSGKGLVYIPKIGDRLDI 63
QY 62 CPRARPPGHSPPNTEFYKLYLVGAQGRRCAPAPNLLITCDRBDLDRFTIKFOEYS 121
DB 64 CPRAEAGRP-----YFYKLYLVPRPQAAACSTVLDPNVLVTCNRPDQEIIRFTIKFOEYS 118
QY 122 PNLMGHFRSHHDYIIATSDGTREGLESLOGGVCLTRGKVLRLVYGSPRGGAVPRKPV 181
DB 119 PNYMGLFEFKKHHDYIITSTNSGLEENREGVCRTKTKIMKVGQDPNAVTPRQLTT 178
QY 182 SEMPERDRGAHSL-PEKENLPDPTSNATSRGAEGPLPPSPMAVAGAAGLA----- 236
DB 179 SRPSKADVTVMATQAPSRGSLGSDGKHETVNOEKSQP-----GASGSSGDDP 231
QY 237 -----LLLLGVAAGAGA-----MCMRRRAKPSBSRHPPGSGFSGSLGL 277
DB 232 GFENSKVALFAAVGAGCVIFLLIIFLVLLKLRKRHRKHTQO-----RAAALSL 282
QY 278 -----GGGGMGPREAREPGEGLIALRGGAADPPFCPHYEKVSQDYGHPYIVODGPPOSP 333
DB 283 STIASPKGSGTAGTEPSDIIILPR---TTENNYCPHYEKVSGDYGHPYIVQEMPPOSP 339
QY 334 PNIYY 338
DB 340 ANIYY 344

RESULT 12
US-10-712-124-60
Sequence 60, Application US/10712124
Publication No. US20040146907A1
GENERAL INFORMATION:
APPLICANT: SMITH, VICTORIA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING DYSPLASIA
FILE REFERENCE: P2000R1
CURRENT APPLICATION NUMBER: US/10/712,124
CURRENT FILING DATE: 2003-11-13
PRIOR APPLICATION NUMBER: US 60/425,813
PRIOR FILING DATE: 2002-11-13
NUMBER OF SEQ ID NOS: 123
SEQ ID NO 60
LENGTH: 346
TYPE: PRT
ORGANISM: Homo sapien
US-10-712-124-60

Query Match 25.4%; Score 623; DB 4; Length 346;
Best Local Similarity 39.2%; Pred. No. 2e-39;
Matches 143; Conservative 48; Mismatches 116; Indels 58; Gaps 9;

QY 8 PGQVAVGALLLLGVGLVSGL-----SLEPYWNSANKRFOAEGGYVLYPOIGDRDL 61
DB 4 PGQWVGKVLVAVVWVALCRLATPLAKNLEPVSWSSLNPKFLSGKGLVYIPKIGDRLDI 63
QY 62 CPRARPPGHSPPNTEFYKLYLVGAQGRRCAPAPNLLITCDRBDLDRFTIKFOEYS 121
DB 64 CPRAEAGRP-----YFYKLYLVPRPQAAACSTVLDPNVLVTCNRPDQEIIRFTIKFOEYS 118

QY 122 PNLMGHFRSHHDYIIATSDGTREGLESLOGGVCLTRGKVLRLVYGSPRGGAVPRKPV 181
DB 119 PNYMGLFEFKKHHDYIITSTNSGLEENREGVCRTKTKIMKVGQDPNAVTPRQLTT 178
QY 182 SEMPERDRGAHSL-PEKENLPDPTSNATSRGAEGPLPPSPMAVAGAAGLA----- 236
DB 179 SRPSKADVTVMATQAPSRGSLGSDGKHETVNOEKSQP-----GASGSSGDDP 231
QY 237 -----LLLLGVAAGAGA-----MCMRRRAKPSBSRHPPGSGFSGSLGL 277
DB 232 GFENSKVALFAAVGAGCVIFLLIIFLVLLKLRKRHRKHTQO-----RAAALSL 282
QY 278 -----GGGGMGPREAREPGEGLIALRGGAADPPFCPHYEKVSQDYGHPYIVODGPPOSP 333
DB 283 STIASPKGSGTAGTEPSDIIILPR---TTENNYCPHYEKVSGDYGHPYIVQEMPPOSP 339
QY 334 PNIYY 338
DB 340 ANIYY 344

RESULT 13
US-10-789-378-30
Sequence 30, Application US/10789378
Publication No. US20050003390A1
GENERAL INFORMATION:
APPLICANT: Axenovitch, Sergey
APPLICANT: Stull, Robert
APPLICANT: Gelman, Marina
APPLICANT: Chui, Kity
APPLICANT: Ng, Dean
TITLE OF INVENTION: DIAGNOSTIC METHODS FOR CANCER DETECTION
FILE REFERENCE: 5189-2
CURRENT APPLICATION NUMBER: US/10/789,378
CURRENT FILING DATE: 2004-02-26
PRIOR APPLICATION NUMBER: 10/441925
PRIOR FILING DATE: 2003-05-19
PRIOR APPLICATION NUMBER: 60/381619
PRIOR FILING DATE: 2002-05-17
PRIOR APPLICATION NUMBER: 60/450886
PRIOR FILING DATE: 2003-02-26
NUMBER OF SEQ ID NOS: 131
SOFTWARE: PatentIn version 3.1
SEQ ID NO 30
LENGTH: 346
TYPE: PRT
ORGANISM: Homo sapiens
US-10-789-378-30

Query Match 25.4%; Score 623; DB 5; Length 346;
Best Local Similarity 39.2%; Pred. No. 2e-39;
Matches 143; Conservative 48; Mismatches 116; Indels 58; Gaps 9;

QY 8 PGQVAVGALLLLGVGLVSGL-----SLEPYWNSANKRFOAEGGYVLYPOIGDRDL 61
DB 4 PGQWVGKVLVAVVWVALCRLATPLAKNLEPVSWSSLNPKFLSGKGLVYIPKIGDRLDI 63
QY 62 CPRARPPGHSPPNTEFYKLYLVGAQGRRCAPAPNLLITCDRBDLDRFTIKFOEYS 121
DB 64 CPRAEAGRP-----YFYKLYLVPRPQAAACSTVLDPNVLVTCNRPDQEIIRFTIKFOEYS 118
QY 122 PNLMGHFRSHHDYIIATSDGTREGLESLOGGVCLTRGKVLRLVYGSPRGGAVPRKPV 181
DB 119 PNYMGLFEFKKHHDYIITSTNSGLEENREGVCRTKTKIMKVGQDPNAVTPRQLTT 178
QY 182 SEMPERDRGAHSL-PEKENLPDPTSNATSRGAEGPLPPSPMAVAGAAGLA----- 236
DB 179 SRPSKADVTVMATQAPSRGSLGSDGKHETVNOEKSQP-----GASGSSGDDP 231
QY 237 -----LLLLGVAAGAGA-----MCMRRRAKPSBSRHPPGSGFSGSLGL 277
DB 232 GFENSKVALFAAVGAGCVIFLLIIFLVLLKLRKRHRKHTQO-----RAAALSL 282

QY 278 ----GGGCGMGPKEAREPGEIGIALRGGAADPPFCPEHYEKVSGDYGHPPYIVODGPPQSP 333
DB 283 STLASPKGSGTAGTGPSPDIIIPLR---TTENNYCPHYEKVSGDYGHPPYIVODGPPQSP 339
QY 334 PNIIY 338
DB 340 ANIIY 344

RESULT 14

US-10-698-907-14
; Sequence 14, Application US/10698907
; Publication No. US20050049194A1

GENERAL INFORMATION:

APPLICANT: Friese, Jonas
APPLICANT: Holmberg, Johan
TITLE OF INVENTION: Use of Ephrine and Related Molecules to Regulate Cellular
FILE REFERENCE: 21882-529 UTIL
CURRENT APPLICATION NUMBER: US/10/698,907
CURRENT FILING DATE: 2003-10-31
PRIOR APPLICATION NUMBER: US 60/460,488
PRIOR FILING DATE: 2003-04-03
PRIOR APPLICATION NUMBER: US 10/291,290
PRIOR FILING DATE: 2002-11-08
PRIOR APPLICATION NUMBER: US 60/393,272
PRIOR FILING DATE: 2002-07-02
PRIOR APPLICATION NUMBER: US 60/345,206
PRIOR FILING DATE: 2001-11-09
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin version 3.2
SEQ ID NO 14
LENGTH: 346
TYPE: PRT
ORGANISM: Homo sapiens
US-10-698-907-14

Query Match

Best Local Similarity 39.2%; Score 623; DB 5; Length 346;
Matches 133; Conservative 48; Mismatches 116; Indels 58; Gaps 9;

QY 8 PGGVGVALLLLGLVLSGL-----SLEPVYVNSANKRFOAEGGYVLPQIGDRLDLL 61
DB 4 PGQWTKVLLVNVVALCRLATPLAKNLEPVSMNLKPLSGKGLVTPKIGDLIDII 63
QY 62 CPBAPRPGHSSSNFYKLYLVGAQGRRCAPAPNLLITCDRPLDLRFTIKQEQYS 121
DB 64 CPBAEAGRP-----YEVYKLYLVPRQAAACSTVLDPNVLVTCNRPEOIRFTIKQEQYS 118
QY 122 PNLMGHPSRSHDYLIATSDGTRREGLESLOGGVCLTRGMKVLLRVGSGPRGAVPRKPV 181
DB 119 PNMGLEPFRKHNDYIITSTNSGSLBGLNREGVCRTKTKLIMKVGDODNAVTPRQLT 178
QY 182 SEMPERDRGAHSLR-PGKENTPCDPTSNATSRGAEGLPPSPMPAVAGAAGLA----- 236
DB 179 SRPSKADLVTKAATGAPSGRSLSDSKHETVNVQEKSGP-----GASGSSGDPD 231
QY 237 -----LLLLGVAAGCA-----MCMRRRAKPSERHPPGSGFRGSGSLGL 277
DB 232 GFENSKVALFAVAGACVIFLLIIFLVLLKLARKHRRKHTQ-----FAAALSL 282
QY 278 ----GGGCGMGPKEAREPGEIGIALRGGAADPPFCPEHYEKVSGDYGHPPYIVODGPPQSP 333
DB 283 STLASPKGSGTAGTGPSPDIIIPLR---TTENNYCPHYEKVSGDYGHPPYIVODGPPQSP 339
QY 334 PNIIY 338
DB 340 ANIIY 344

RESULT 15
US-09-754-105-2
; Sequence 2, Application US/09754105

; Patent No. US20010009768A1

GENERAL INFORMATION:

APPLICANT: Cerretti, Douglas
APPLICANT: Reddy, Prabhitha
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING CYTOKINE DESIGNATED LERK-5
FILE REFERENCE: 28232
CURRENT APPLICATION NUMBER: US/09/754,105
CURRENT FILING DATE: 2001-01-03
PRIOR APPLICATION NUMBER: 09/329,531
PRIOR FILING DATE: 1998-06-10
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin version 3.0
SEQ ID NO 2
LENGTH: 333
TYPE: PRT
ORGANISM: homo sapiens
US-09-754-105-2

Query Match

Best Local Similarity 40.5%; Score 620.5; DB 3; Length 333;
Matches 133; Conservative 52; Mismatches 130; Indels 13; Gaps 5;

QY 14 GALLILGLVLSGLSLEPVYVNSANKRFOAEGGYVLPQIGDRLDLLCPRARPPGPHS 73
DB 14 GVLMLVCRTALSKSIVLEBIYVNSNSKFLPGQGLVLPQIGDKLIDICPKV---DSKTV 70
QY 74 PVYEFYKLYLVGAQGRCEAPAPNLLITCDRPLDLRFTIKFOEYSPNLKGHEFRSH 133
DB 71 GQYEFYKLYLVWDKQDQDRCTIKKENTPLNCKAKPQODIKFTIKFOEYSPNLKGLEFQK 130
QY 134 DYIITSDGTRREGLESLOGGVCLTRGMKVLLRVGO--SPRGAVPRKPEVSEMPMER-DR 190
DB 131 DYIITSTNSGSLBGLDNREGVCQTRAMKILMKVGDASASASTNKDPTREBELAGTN 190
QY 191 GAHSLPEKENTLPDPTSNATSRGAEGLPPSPMPAVAGAAGLALLLGVAGAGAMC 250
DB 191 GRSSTSPVKNPQSGSTDGNSAGHGNILGSEVALFAGIASGCIPIFVITITLVLL 250
QY 251 WRRRAKPSERHPPGSGFRGSGSLGIGGCGMGPKEAREPGEIGIALRGGAADPPFCPH 310
DB 251 KYRRHRKHSPOHTTTTSLSTLATPRGSGNN---NGSEPSDIIIPLR---TADSVFCPH 303
QY 311 YEKVSGDYGHPPYIVODGPPQSPPNIIY 338
DB 304 YEKVSGDYGHPPYIVODGPPQSPANIIY 331

Search completed: December 21, 2005, 14:41:50
Job time: 130.201 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 21, 2005, 14:21:53 ; Search time 176.277 Seconds
(without alignments)
1821.088 Million cell updates/sec

Title: US-10-021-121-2
Perfect score: 2450
Sequence: 1 MGPSPHSGPGVWGAALLILG.....TTLLRGRASVEAAGHGPEL 455

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1841	75.1	340	1 EFN83_HUMAN	Q15768 homo sapien
2	1771	72.3	340	1 EFN83_MOUSE	Q35193 mus musculu
3	1771	72.3	340	2 O5P221_MOUSE	O5P221 mus musculu
4	914	37.3	331	2 Q90231_BRABE	Q90231 brachydanto
5	914	37.3	342	2 Q502Q3_BRABE	Q502Q3 brachydanto
6	910	37.1	327	2 Q9P769_XENLA	Q9P769 xenopus lae
7	628.5	25.7	336	1 EFN82_MOUSE	P52800 mus musculu
8	628.5	25.7	336	2 Q4F3M3_MOUSE	Q4F3M3 mus musculu
9	623	25.4	346	1 EFN81_HUMAN	P98172 homo sapien
10	620.5	25.3	333	1 EFN82_HUMAN	P52799 homo sapien
11	620.5	25.3	333	2 Q5JY56_HUMAN	Q5JY56 homo sapien
12	620.5	25.3	333	2 Q9PUJ4_CHICK	Q9PUJ4 gallus gall
13	619	25.3	334	1 EFN81_CHICK	Q73612 gallus gall
14	617.5	25.2	332	1 EFN82_BRABE	Q73874 brachydanto
15	607	24.8	341	2 Q90233_BRABE	Q90233 brachydanto
16	606.5	24.8	345	1 EFN81_MOUSE	Q6P7B6 rattus norv
17	604.5	24.7	345	1 EFN81_MOUSE	P52795 mus musculu
18	604.5	24.7	345	1 EFN81_MOUSE	P52795 mus musculu
19	599.5	24.5	345	1 EFN81_MOUSE	P52795 mus musculu
20	596.5	24.3	329	2 Q6P553_XENLA	Q6P553 xenopus lae
21	596.5	24.3	334	2 Q90232_CHICK	Q90232 brachydanto
22	591	24.1	327	1 EFN81_XENLA	Q13097 xenopus lae
23	559.5	22.8	324	2 Q4SHZ6_TETNG	Q4SHZ6 tetraodon n
24	443	18.1	324	2 Q4T7D5_TETNG	Q4T7D5 tetraodon n
25	401	16.4	359	2 Q4R8K3_TETNG	Q4R8K3 tetraodon n
26	349.5	14.3	359	2 Q4H318_CIOIN	Q4H318 ciona intes
27	341.5	13.9	217	2 Q5UT57_HUMAN	Q5UT57 homo sapien
28	331	13.5	205	2 Q9W6H9_XENLA	Q9W6H9 xenopus lae
29	251.5	10.3	97	2 Q9RD21_TETNG	Q9RD21 tetraodon n
30	239.5	9.8	212	2 Q61WH3_CAEBR	Q61WH3 caenorhabd
31	234	9.6	218	2 Q9U3M2_CAEBL	Q9U3M2 caenorhabd

32	205	8.4	182	2 Q4RT95_TETNG	Q4RT95 tetraodon n
33	198.5	8.1	279	2 Q9U474_CAEBL	Q9U474 caenorhabd
34	198	8.1	278	2 Q61HF9_CAEBR	Q61HF9 caenorhabd
35	192	7.8	652	2 Q9V4E1_DROME	Q9V4E1 drosophila
36	185	7.6	195	1 EFN82_BRABE	P79727 brachydanto
37	184.5	7.5	428	2 Q5TXC6_ANOGA	Q5TXC6 anopheles g
38	182	7.4	260	1 Q6VU49_MANSE	Q6VU49 manduca sex
39	179	7.3	238	1 EFN83_HUMAN	P52797 homo sapien
40	178.5	7.3	202	2 Q98RT21_CHICK	Q98RT21 gallus gall
41	176	7.2	209	1 EFN82_MOUSE	P52801 mus musculu
42	175.5	7.2	213	1 EFN82_HUMAN	Q43921 homo sapien
43	172.5	7.0	217	2 Q5MTP3_XENTR	Q5MTP3 xenopus tro
44	172	7.0	200	1 EFN82_CHICK	P52802 gallus gall
45	170.5	7.0	228	1 EFN85_CHICK	P52804 gallus gall

ALIGNMENTS

RESULT 1
EFN83_HUMAN STANDARD: PRT: 340 AA.
ID Q15768; Q00680; Q81BH7; Q92875;
AC Q15768; Q00680; Q81BH7; Q92875;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE EPHrin-B3 precursor (EPH-related receptor tyrosine kinase ligand 8)
DE (LEK-8) (EPH-related receptor transmembrane ligand ELK-L2).
GN Name=EFN83; Synonyms=EPH8; LEK8;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Cerretti D.P.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC Tissue=Brain;
RX MEDLINE=97271551; PubMed=9126477; DOI=10.1006/geno.1997.4615;
RA Tang X.X., Pleasure D.E., Ikegaki N.;
RT "CDNA cloning, chromosomal localization, and expression pattern of
RT EPH8, a new member of the EPH gene family encoding ligands of EPH-
RT related protein-tyrosine kinase receptors.";
RL Genomics 41:17-24(1997).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC Tissue=Brain cortex;
RX MEDLINE=96404527; PubMed=8808709;
RA Gale N.W., Flemmiken A., Compton D.C., Jenkins N.A., Copeland N.G.,
RA Gilibert D., Davis S., Wilkinson D.G., Yancopoulos G.D.;
RT "Elk-13, a novel transmembrane ligand for the Eph family of receptor
RT tyrosine kinases, expressed in embryonic floor plate, roof plate and
RT hindbrain segments.";
RL Oncogene 13:1343-1352(1996).
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC Tissue=Brain;
RX MEDLINE=2238827; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Scheafer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Miall S.J.,
RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Guatarte P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultyk S.W.,
RA Villalón D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
FAhey J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J.W., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smalhus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RT [5]
 RN PROTEIN SEQUENCE OF 28-42.
 RP PubMed:15340161; DOI=10.1101/ps.04682504;
 RX Zhang Z., Henzel W.J.;
 RA "Signal peptide prediction based on analysis of experimentally
 RT verified cleavage sites";
 RL Protein Sci. 13:2819-2824(2004).
 [6]
 RN INTERACTIONS WITH GRIP1 AND GRIP2.
 RP TISSUE=Fetal brain;
 RC MEDLINE=99211388; PubMed=10197531; DOI=10.1016/S0896-6273(00)80706-0;
 RA Brueckner K., Pablo Labrador J., Scheiffele P., Herd A., Seeburg P.H.,
 RA Klein R.;
 RT "Ephrin ligands recruit GRIP family PDZ adaptor proteins into raft
 RT membrane microdomains";
 RL Neuron 22:511-524(1999).
 CC -1- FUNCTION: May play a pivotal role in forebrain function. Binds to,
 CC and induce the collapse of, commissural axons/growth cones in
 CC vitro. May play a role in constraining the orientation of
 CC longitudinally projecting axons (By similarity).
 CC -1- SUBUNIT: Interacts with GRIP1 and GRIP2.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: Highly expressed in brain; expressed in
 CC embryonic floor plate, roof plate and hindbrain segments.
 CC -1- SIMILARITY: Belongs to the ephrin family.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 DR EMBL, U57001; AAB05170.1; -; mRNA.
 DR EMBL, U66406; AAC51203.1; -; mRNA.
 DR EMBL, U62775; AAC50707.1; -; mRNA.
 DR EMBL, BC022499; AAH22499.1; -; mRNA.
 DR EMBL, BC042944; AAH42944.1; -; mRNA.
 DR HSSP: P52800; 1IKO.
 DR EMBL, ENSG00000108947; Homo sapiens.
 DR HGNC: HGNC:3228; EFN3.
 DR MIM: 602297; -;
 DR GO: GO:0005887; C:integral to plasma membrane; TAS.
 DR GO: GO:0005005; P:transmembrane-ephrin receptor activity; TAS.
 DR GO: GO:0007267; P:cell signaling; TAS.
 DR GO: GO:0007399; P:neurogenesis; TAS.
 DR InterPro: IPR001799; Ephrin.
 DR Pfam: PF00812; Ephrin; 1.
 DR PRINTS: PRO1347; EPHRIN.
 DR ProDom: PD002533; Ephrin.
 DR PROSITE: PS01299; EPHRIN; 1.
 KW Developmental protein; Differentiation; Direct protein sequencing;
 KW Glycoprotein; Neurogenesis; Polymorphism; Signal; Transmembrane.
 FT SIGNAL 1 27
 FT CHAIN 28 340 Ephrin-B3.
 FT TOPO_DOM 28 226 Extracellular (Potential).
 FT TRANSMEM 227 247 Potential.
 FT TOPO_DOM 248 340 Cytoplasmic (Potential).
 FT MOTIF 338 340 PDZ recognition motif (Potential).
 FT CARBOHYD 210 210 N-linked (GlcNAc...) (Potential).
 FT DISULFID 62 104 By similarity.
 FT DISULFID 92 156 R -> O.
 FT VARIANT 166 166 /FTID=VAR_002356.
 SEQUENCE 340 AA; 35835 MW; EDFPZAZ3CFDE79F CRC64;

Query Match 75.1%; Score 1641; DB 1; Length 340;
 Best Local Similarity 100.0%; Pred. No. 1e-110;
 Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGPPHSGPGGVVGLLLGLVGLVGLSLPEVYNNNAKRFOAGGYLVLPQIDRLD 60
 DB 1 MGPPHSGPGGVVGLLLGLVGLVGLSLPEVYNNNAKRFOAGGYLVLPQIDRLD 60
 QY 61 LCPRARPPGPHSSPYVEFYKYLTVGAQGRRCCEAPAPNLLTCDRDLDFTKFOEY 120
 DB 61 LCPRARPPGPHSSPYVEFYKYLTVGAQGRRCCEAPAPNLLTCDRDLDFTKFOEY 120
 QY 121 SPNLWGEHFRSHDYIITATSGTBEGLSLGGVCLTGMKVLRLVQSGPRGAVPRKP 180
 DB 121 SPNLWGEHFRSHDYIITATSGTBEGLSLGGVCLTGMKVLRLVQSGPRGAVPRKP 180
 QY 181 VSEPMERDGAHSLPECKENLPDPTSNATSRGAEGLPPSPMPAVGAAGGLALLL 240
 DB 181 VSEPMERDGAHSLPECKENLPDPTSNATSRGAEGLPPSPMPAVGAAGGLALLL 240
 QY 241 GVAGAGGAMCWRRRRAKSESHPGSPFGSGSLGLGGGGMGPRAEPGEIGIALRGG 300
 DB 241 GVAGAGGAMCWRRRRAKSESHPGSPFGSGSLGLGGGGMGPRAEPGEIGIALRGG 300
 QY 301 GAADPPCPHYEKVSGDYGHPYIYVODGPPGSPNNIY 338
 DB 301 GAADPPCPHYEKVSGDYGHPYIYVODGPPGSPNNIY 338
 RESULT 2
 EFN3 MOUSE STANDARD; PRT; 340 AA.
 ID EFN3 MOUSE
 AC 035393;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Ephrin-B3 precursor.
 GN Name=Efnb3;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=98143367; PubMed=9484836; DOI=10.1038/91.pnc.1201557;
 RA Bergemann A.D., Zhang L., Chiang M.-K., Brandtilla R., Klein R.,
 RA Flanagan J.G.;
 RT "Ephrin-B3, a ligand for the receptor EphB3, expressed at the midline
 RT of the developing neural tube";
 RL Oncogene 16:471-480(1998).
 [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buterow K.H., Schaefer C.F., Hsieh F.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Pangue C.,
 RA Raha S.S., Iqbal N.A., Peters G.J., Abramson R.D., Mollath S.J.,
 RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Viallon D.K., Muny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smalhus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP FUNCTION:
 RX MEDLINE=20171264; PubMed=10704386;
 RA Imondil R., Wideman C., Kaprielian Z.;
 RT Complementary expression of transmembrane ephrins and their receptors
 RT in the mouse spinal cord: a possible role in constraining the
 RT orientation of longitudinally projecting axons.";
 RL Development 127:1397-1410(2000).
 CC -1- FUNCTION: May play a pivotal role in forebrain function. Binds to,
 CC and induce the collapse of, commissural axons/growth cones in
 CC vitro. May play a role in constraining the orientation of
 CC longitudinally projecting axons.
 CC -1- SUBUNIT: Interacts with GRIP1 and GRIP2 (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: Expressed on lateral floor plate cells,
 CC specifically on commissural axon segments that have passed through
 CC the floor plate. Expressed in cells of the retinal ganglion cell
 CC layer during retinal axon guidance to the optic disk.
 CC -1- DEVELOPMENTAL STAGE: Expressed in the floor plate throughout the
 CC period of commissural axon pathfinding.
 CC -1- SIMILARITY: Belongs to the ephrin family.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL, AF025288; AAC53537.1; -; mRNA.
 CC EMBL, BC052001; AAH52001.1; -; mRNA.
 CC EMBL, BC058617; AAH58617.1; -; mRNA.
 CC HSSP; P52800; IIRK.
 CC Ensembl; ENSMUSG00000003934; Mus musculus.
 CC DR MGI; MGI:109196; Efnb3.
 CC DR GO; GO:0005615; Cytoplasmic space; TAS.
 CC DR GO; GO:0016021; Cytoplasm to membrane; TAS.
 CC DR GO; GO:0007626; P:adult walking behavior; IMP.
 CC DR GO; GO:0016198; P:axon choice point recognition; IMP.
 CC DR InterPro; IPR001799; Ephrin, 1.
 CC DR Pfam; PF00812; Ephrin, 1.
 CC DR PRINTS; PR01347; EPHRIN.
 CC DR ProDom; PD002533; Ephrin, 1.
 CC DR PROSITE; PS01299; EPHRIN, 1.
 CC KW Developmental protein; Differentiation; Glycoprotein; Neurogenesis;
 CC Signal; Transmembrane.
 CC FT SIGNAL 1 27 Potential.
 CC FT CHAIN 28 340 Ephrin-B3.
 CC FT TOPO_DOM 28 227 Extracellular (Potential).
 CC FT TRANSMEM 228 248 Potential.
 CC FT TOPO_DOM 249 340 Cytoplasmic (Potential).
 CC FT MOTIF 338 340 PDZ recognition motif (Potential).
 CC FT CARBOHYD 210 210 N-linked (GlcNAc...) (Potential).
 CC FT DISULFID 62 104 By similarity.
 CC FT DISULFID 92 156 By similarity.
 CC SEQUENCE 340 AA; 35885 MW; 52F3D58FD209A6B8 CRC64;
 SQ
 Query Match 72.3%; Score 1771; DB 1; Length 340;
 Best Local Similarity 95.6%; Pred. No. 3.4e-106;
 Matches 323; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

DB 121 SPNLWGHFRSHHDYIATSDGTREGLESLOGVCLTRGMKYLVRVGS PRGAVPRKP 180
 QY 181 VSEMPERDGAASHLEPKENLPDPTSNATSRGAEPPLPPSPVAVGAGLALLLL 240
 DB 181 VSEMPERDGAASHLEPKENLPDPTSNATSRGAEPPLPPSPVAVGAGLALLLL 240
 QY 241 GVAGAGAMCWRRRRAKPSRRHPGSGFSGGSLGCGGCMGPPEAPFGLIALRG 300
 DB 241 GVAGAGAMCWRRRRAKPSRRHPGSGFSGGSLGCGGCMGPPEAPFGLIALRG 300
 QY 301 GAADPPFCHEYENSGDYHPYTYVDGPPSPPNITY 338
 DB 301 GAADPPFCHEYENSGDYHPYTYVDGPPSPPNITY 338
 RESULT 3
 ID Q5F221_MOUSE PRELIMINARY; PRT; 340 AA.
 AC Q5F221;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE Ephrin B3 (16 days embryo head cDNA, RIKEN full-length enriched
 DE library, clone:CI30048B01 product:m-ephrin-B3).
 GN Name=Efnb3; ORFNames=RP23-56120.5-001;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Tromans A.;
 RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Aikawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K. I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadoya K., Matsuda H. A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuenli P., Lewis S., Matsumoto Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L. M., Staudl F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okita T., Furuno M., Aono H., Baldarelli R., Bash G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M. F.,
 RA Brownstein M. J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D. A., Kamya M., Lee N. H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Komabaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata K., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K. H., Weitz C., Whitaker C., Wilming L.,
 RA Wymbs-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohseki S.,
 RA Hayashizaki Y.,
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 403:685-690(2001).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kiyosawa H.,
 RA Nishida K., Oshino N., Saito R., Suzuki R., Yamana K. I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D. P., Bult C., Hume D. A., Quackenbush J.,

RA Schirnl LM, Kanapin A., Marcuza H., Batilov S., Belser K.W.,
 RA Blake U.A., Bradt D., Bruscia V., Chochia C., Corbani L.B., Cousins S.,
 RA Datta E., Dregan T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmeron S., Guecinich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawasaki H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Kanagaya A., Kurochkin I.V., Lee Y., Lemhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie B., Miki H.,
 RA Nagashima T., Numa K., Okido T., Pavan W.J., Petrea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.V., Qi D., Ramachandran S.,
 RA Hironaka-Tsukikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiroki T., Maki K., Kawai J., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Saeki D., Shibata K., Shinagawa A.,
 RA Yaunishi A., Yoshino Y., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.,
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.",
 RL Nature 420:563-573(2002).
 [5]
 RA Nucleotide sequence.
 RP STRAIN=C57BL/6J; TISSUE=Head;
 RC MEHLIN=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RX Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.",
 RL Genome Res. 10:1617-1630(2000).
 [6]
 RA Nucleotide sequence.
 RP STRAIN=C57BL/6J; TISSUE=Head;
 RC MEHLIN=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RX Shibata K., Itoh M., Aizawa K., Nagao S., Saeki N., Carninci P.,
 RA Konno H., Akiyama Y., Nishi K., Kitsumi T., Tashiro H., Itoh M.,
 RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.",
 RL Genome Res. 10:1757-1771(2000).
 [7]
 RA Nucleotide sequence.
 RP STRAIN=C57BL/6J; TISSUE=Head;
 RC Adachi J., Aizawa K., Akimura K., Akikawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kaubawa T.,
 RA Kozaki H., Kawai J., Kojima Y., Kondo S., Konno H., Kondo H., Koya S.,
 RA Kurihara C., Matsumura T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Saeki D., Shibata K., Shinagawa A., Shiroki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toy T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
 RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AL731687; CAIS2012.1; -- genomic DNA.
 DR EMBL; AK048305; BAC3229.1; -- gRNA.
 SO SEQUENCE 340 AA; 35864 MW; 52F3D58FD209A6B8 CRC64;

Db	1	MGAFHFGGCVQVAGALLLLGFAAGLVGSLSEPPYWNANSNKR	FOABEGVYLVPOIGDRDL	60
Qy	61	LCPPARPPGPHSSPNVEFFYKYLIVGAGAGRRCEAP	PAPNLLLTCDRPLDLRFTTKFOEY	120
Db	61	LCPPARPPGPHSSPNVEFFYKYLIVGAGAGRRCEAP	PAPNLLLTCDRPLDLRFTTKFOEY	120
Qy	121	SPNMGHFRHNDHYIITATSDGTREGLEST	OGGVCLTRGMKULLRVQSPRGGAVPKRP	180
Db	121	SPNMGHFRHNDHYIITATSDGTREGLEST	OGGVCLTRGMKULLRVQSPRGGAVPKRP	180
Qy	181	VSEMPMERDRKAASLSLEGKENTLPGDPTSNATSRGAEGLP	PPSPMFAVAGAAAGLALLLL	240
Db	181	VSEMPMERDRKAASLSLEGKENTLPGDPTSNATSRGAEGLP	PPSPMFAVAGAAAGLALLLL	240
Qy	241	GVAGAGGAMCWRRRARRKESRSRHPFGSGSLGLGSGGGMGP	REAREPGEGLIALTRGG	300
Db	241	GVAGAGGAMCWRRRARRKESRSRHPFGSGSLGLGSGGGMGP	REAREPGEGLIALTRGG	300
Qy	301	GAADPPFCPHYEXVSGDYGHVYTVQGGPPSPPIYY	338	
Db	301	GTADPPFCPHYEXVSGDYGHVYTVQGGPPSPPIYY	338	
RESULT 4				
ID	Q90231	BRARE	PRELIMINARY;	PRT; 331 AA.
AC	Q90231;			
DT	01-DEC-2001	(TREMBLrel. 19, Created)		
DT	01-DEC-2001	(TREMBLrel. 19, Last sequence update)		
DT	01-OCT-2003	(TREMBLrel. 25, Last annotation update)		
DE	Ephrin B3.			
GN	Name=efnb3;			
OS	Brachydanio rerio (zebrafish) (Danio rerio).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;			
OC	Cyprinidae; Danio.			
OX	NCBI_TaxID=7955;			
RN	[1]			
RP	NCLEOTIDE SEQUENCE.			
RX	MEDLINE=21290827; PubMed=11397014; DOI=10.1006/dbio.2001.0281;			
RA	Chan J., Mabry J.D., Serluca F.C., Chen J.N., Goldstein N.B.,			
RA	Thomas M.C., Cleary J.A., Brennan C., Fishman M.C., Roberts T.M.,			
RT	"Morphogenesis of prechordal plate and notochord requires intact			
RT	epm/ephrin b signaling."			
RL	Dev. Biol. 234:470-482(2001).			
DR	EMBL; AF375227; AAK64277.1; -. mRNA.			
DR	HSSP; P52800; IIKO.			
DR	Ensembl; ENSDARG0000008177; Danio rerio.			
DR	ZFIN; ZDB-GENE-010618-3; efnb3.			
DR	GO; GO:0016020; C:membrane; IEA.			
DR	InterPro; IPR001799; Ephrin.			
DR	Pfam; PF00812; Ephrin. 1.			
DR	PRINTS; PR01347; EPHRIN.			
DR	ProDom; PD002533; Ephrin; 1.			
DR	PROSITE; PS01293; EPHRIN; 1.			
SQ	SEQUENCE 331 AA; 35638 MW; 645EACD509A09818 CRC64;			
Query Match 37.3%; Score 914; DB 2; Length 331;				
Best Local Similarity 54.5%; Pred. No. 5.4e-51;				
Matches 188; Conservative 43; Mismatches 74; Indels 40; Gaps 10				
Qy	10	GVRVGALLLLGLVGLVSGLSLEPYWNSANKRFQABGGVTVLPQIGDRDL	LCPPARPPG	69
Db	9	GLGILITFLVYDLG-ITATNNMEPIYWSLNKRFSDDKGVYLVPOIGDRDL	LCPSDPPG	67
Qy	70	PHSSNVEFFYKYLIVG-AGRRCEAPAPNLLLTCDRPLDLRFTTKFOEYSPNMGH		128
Db	68	PRAAPADYVYKYLIVSSREQADRCVEVGAPNLLLTCDRPNSDMRFTTKFOEYSPNMGH		127
Qy	129	FRSHDYYIITATSDGTREGLESTOGGVCLTRGMKULLRVQSPRG-GAVPRKPVSEMPWE		187
Db	128	FKTNHDYIITATSDGTREGLESMRGGVCAATGCMKVLAVGQSPYGLPAKSPKPDs-----		182


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QY 188 RRGAAHSLPEKENTPGDPTSNAT-----SRGAEGLPPSPMPAVAGAAGLALL 239
DB 183 -----AGRINPNPCTGNSTHPQIPPRSGGEMNGLPASNIAVIAAGGSAFLL 232
QY 240 LGVAGAGAMCWMRRRAKPSSESHHPGSGFG-----RGSLGLGGGGGMPREABEGEL 293
DB 233 L-VTAVICVVCYRRRAKSHSHHP-PLSLSLTSPKRCGGCGGCGGNNNG---SEPSDI 287
QY 294 GIALRGGAADPPFCPHYKVSQDYGHPYIYVODGPPSPNITY 338
DB 288 IIFLR---TSDSAVCPHYKVSQDYGHPYIYVODGPPSPNITY 329

RESULT 5
050203 BRARE
ID 050203_BRARE PRELIMINARY; PRT; 342 AA.
AC 050203;
DT 13-SEP-2005 (TReMBLrel. 31, Created)
DT 13-SEP-2005 (TReMBLrel. 31, Last sequence update)
DE 13-SEP-2005 (TReMBLrel. 31, Last annotation update)
DE Efnb3 protein.
GN Name:efnb3;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_Taxid=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schlier G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkin R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Lottelkamp N.A., Peters G.J., Abramson R.D., Millar S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richardson D., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Murray D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Feherty J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RG NIH MGC Project;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL, BC095605, AAH95605.1, -, mRNA.
SQ SEQUENCE 342 AA; 36885 MW; 1629532234F85386 CRC64;

Query Match
Best Local Similarity 54.5%; Score 914; DB 2; Length 342;
Matches 188; Conservative 43; Mismatches 74; Indels 40; Gaps 10;

QY 10 GYRVALLLLGLVGLSLSPVYNSANKRFQABEGGYLYPOIGDRDLDCPRARPPG 69
DB 20 GIGILILIFVLDLIG-ITATNMEPIYNNNSKRSDKGYLYLPQIDRLDLICPSSDPG 78
QY 70 PHSSPYEFYKLYLVGG-AQGRCEAPAPNLLTCDRPLDLRFTIKFOEYSPNLMGHE 128
DB 79 PRAPADYEYKLYLVSSREDARCEVYTGAPNLLTCDKRPSSDKRFTIKFOEYSPNLMGHE 138
QY 129 FRSNHDYIATSQTRGGLSLGGVCLTRGMKVLRLVQGSPPG-GAVPRKEVSEMPME 187
DB 129 FRSNHDYIATSQTRGGLSLGGVCLTRGMKVLRLVQGSPPG-GAVPRKEVSEMPME 187

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DB 139 FKTNDHYFIATSQTRGGLSLGGVCLTRGMKVLRLVQGSPPGPAKSPKDS----- 193
QY 188 RRGAAHSLPEKENTPGDPTSNAT-----SRGAEGLPPSPMPAVAGAAGLALL 239
DB 194 -----AGRINPNPCTGNSTHPQIPPRSGGEMNGLPASNIAVIAAGGSAFLL 243
QY 240 LGVAGAGAMCWMRRRAKPSSESHHPGSGFG-----RGSLGLGGGGGMPREABEGEL 293
DB 244 L-VTAVICVVCYRRRAKSHSHHP-PLSLSLTSPKRCGGCGGCGGNNNG---SEPSDI 298
QY 294 GIALRGGAADPPFCPHYKVSQDYGHPYIYVODGPPSPNITY 338
DB 299 IIFLR---TSDSAVCPHYKVSQDYGHPYIYVODGPPSPNITY 340

RESULT 6
09PT69 XENLA
ID 09PT69_XENLA PRELIMINARY; PRT; 327 AA.
AC 09PT69;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Ephrin-B3 precursor.
GN Ephrin-B3 precursor.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Cranata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_Taxid=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryonic head;
RX MEDLINE=2009673; PubMed=10633856;
RA Hei10.1002/(SICI)1097-0177(199912)216:4/5<361::AID-DVNY3.0.CO;2-W;
RA Wolking P.M., Brandt D.M.E., Robinson V., Christensen J.H.,
RA Wilkison D.G., Brandt A.W.;
RT "Comparative analysis of embryonic gene expression defines potential
RT interaction sites for Xenopus EphA4 receptors with ephrin-B ligands.";
RL Dev. Dyn. 216:361-373(1999).
DR EMBL, AJ236866; CAB65511.1, -, mRNA.
DR HSSP, P52800; IIKO.
DR GO, GO:0016020; C:membrane, IEA.
DR InterPro, IPR002086; Aldehyde dehydrog.
DR InterPro, IPR001799; Ephrin.
DR Pfam, PF006812; Ephrin.1.
DR PRINTS, PR01347; EPHRIN.
DR PRODOM, PD002533; Ephrin.1.
DR PROSITE, PS00687; ALDEHYDE DEHYDR. GLU; UNKNOWN_1.
DR PROSITE, PS01299; EPHRIN.1.
DR Signal.
FT SIGNAL.
SQ SEQUENCE 327 AA; 35913 MW; 4BB0FA39D4C22DCC CRC64;

Query Match
Best Local Similarity 37.1%; Score 910; DB 2; Length 327;
Matches 190; Conservative 30; Mismatches 82; Indels 14; Gaps 8;

QY 25 VEGLSLSEPYVNSANKRFQABEGGYLYPOIGDRDLDCPRARPPGSHSPNTEFYLYV 84
DB 22 ISALSLDPIYVNSNKRFEFTGEGYLYPOIGDRDLDCPRSEBPGFSSPEYLYLYV 81
QY 85 GGAOG-RCEAPAPAPNLLTCDRPLDLRFTIKFOEYSPNLMGHEFRSHHDYIATSQD 143
DB 82 GKREKSSCSILRTPNLLTCDRPSODLRFITKFOEFSNLMGHEFGSQRDYIATSQD 141
QY 144 TRGGLSLGGVCLTRGMKVLRLVQGSPPGAVPRKPVSEMPMEHRAHSL-EPGEN 202
DB 142 TMDGIEITLGGVCEFGKMYTLKVGSPVGAATPPRRPS---AGKDSGISPVMPDIPN 198
QY 203 LPQDPTSNATSRGAGPLPPSPMPAVAGAAGLALLLGVAGAGAMCWMRRRAKPSSE 262
DB 199 V-GETSGNATYKQGENGLPISHVPLVAGAAGLALLL-VFGVGVAVCHRRRAKSDTR 256
QY 263 HPGPGSFRGSGSLGLGGGGMGPREABEGELIALRGGAADPPFCPHYKVSQDYGHPV 322

```

Db 257 HP-PLSLGISTPKRGKGN-----NGHEPEDIIMPLRPSAG--AFCPHYEKVSGDHPV 309
 Oy 323 YIVODGPQSPNNITY 338
 Db 310 YIVODMASQSPNNITY 325

RESULT 7
 EPNB2 MOUSE
 ID EPNB2 MOUSE STANDARD; PRT; 336 AA.
 AC P52807;
 DT 01-OCT-1996 (rel. 34, Created)
 DT 01-OCT-1996 (rel. 34, Last sequence update)
 DT 10-MAY-2005 (rel. 47, Last annotation update)
 DE Ephrin-B2 precursor (EPH-related receptor tyrosine kinase ligand 5)
 DE (LEKX-5) (HTK ligand) (HTK-L) (ELF-2)
 GN Name=ELFb2; Synonyms=ELF2, Epl5, Epl95, Hck1, Lerk5;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 NCBI_TaxId=10090;
 (1)
 NUCLEOTIDE SEQUENCE.
 RP MEDLINE=96145238; PubMed=8559144; DOI=10.1016/0161-5890(95)00108-5;
 RX Cerretti D.P., Vanden Boe T., Nelson N., Kozlosky C.J., Reddy P.,
 RA Maraskovsky E., Park L.S., Lyman S.D., Copeland N.G., Gilbert D.J.,
 RA Jenkins N.A., Fletcher R.A.;
 RT Isolation of LEKX-5: a ligand of the eph-related receptor tyrosine
 RT kinases.";
 RT Mol. Immunol. 32:1197-1205(1995).
 (2)
 NUCLEOTIDE SEQUENCE.
 RP STRAIN=CB57BL/6J X SJL/J;
 RX MEDLINE=9519254; PubMed=7534404;
 RA Bennett B.D., Zeigler F.C., Gu Q., Fendly B., Goddard A.D.,
 RA Gillett N., Matthews W.;
 RT Molecular cloning of a ligand for the EPH-related receptor protein-
 RT tyrosine kinase Hk.";
 RT Proc. Natl. Acad. Sci. U.S.A. 92:1866-1870(1995).
 (3)
 NUCLEOTIDE SEQUENCE.
 RP STRAIN=ICR; TISSUE=Brain;
 RX MEDLINE=95379837; PubMed=7651410;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo W.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mallaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richardson S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Murzy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN (5)
 RP FUNCTION.
 RX MEDLINE=20171264; PubMed=10704386;
 RA Mondini R., Wideman C., Kaprielian Z.;
 RT "Complementary expression of transmembrane ephrins and their receptors
 RT in the mouse spinal cord: a possible role in constraining the
 RT orientation of longitudinally projecting axons.";
 RL Development 127:1397-1410(2000).
 (6)
 RN X-RAY CRYSTALLOGRAPHY (1.92 ANGSTROMS) OF 30-170-
 RP PubMed=11703926; DOI=10.1016/S1534-5807(01)00002-8;
 RX Toth J., Cutforth T., Gellinas A.D., Bethoney K.A., Bard J.,
 RA Harrison C.J.;
 RT "Crystal structure of an ephrin ectodomain.";
 RL Nature 414:933-938(2001).
 (7)
 RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 31-168 IN COMPLEX WITH EPHB2.
 RX PubMed=11780069; DOI=10.1038/414933a;
 RA Hämnen J.-P., Rajashankar K.R., Lackmann M., Cowan C.A.,
 RA Henkemeyer M., Nikolov D.B.;
 RT "Crystal structure of an Eph receptor-ephrin complex.";
 RL Nature 414:933-938(2001).
 CC -1- FUNCTION: Binds to the receptor tyrosine kinases EPNB2 and EPNB4.
 CC May play a role in constraining the orientation of longitudinally
 CC projecting axons.
 CC -1- SUBUNIT: Interacts with PDZRN3 (By similarity). Binds to the
 CC receptor tyrosine kinase EPNB4.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: Expressed on lateral floor plate cells,
 CC specifically on commissural axon segments that have passed through
 CC the floor plate. Expressed in cells of the retinal ganglion cell
 CC layer during retinal axon guidance in the floor plate throughout the
 CC -1- DEVELOPMENTAL STAGE: Expressed in the floor plate throughout the
 CC period of commissural axon pathfinding.
 CC -1- PTM: Inducible phosphorylation of tyrosine residues in the
 CC cytoplasmic domain (By similarity).
 CC -1- SIMILARITY: Belongs to the ephrin family.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL: U16819; AAA9708.1; -; mRNA.
 CC EMBL: U38847; AAC42052.1; -; mRNA.
 CC EMBL: U30244; AAA82934.1; -; mRNA.
 CC EMBL: BC057009; AAH57009.1; -; mRNA.
 CC PIR: I49766; I49766.
 CC PDB: 1IKO; X-ray; P=30-207.
 CC PDB: 1KGY; X-ray; E/F/G/H=31-168.
 CC DR Ensembl: ENSMUSG0000001300; Mus musculus.
 CC MGI: MGI:105097; Efnb2.
 CC GO: GO:0005615; C:extracellular space; TAS.
 CC GO: GO:0016021; C:integral to membrane; TAS.
 CC GO: GO:0005886; C:plasma membrane; IDA.
 CC GO: GO:0005515; F:protein binding; IPI.
 CC GO: GO:0001945; P:lymph vessel development; IMP.
 CC GO: GO:0009887; P:organogenesis; IMP.
 CC InterPro: IPR001799; Ephrin.
 CC Pfam: PF00812; Ephrin.1.
 CC PRINTS: PR01347; EPHRN.
 CC Prodom: PD002533; Ephrin.1.
 CC PROSITE: PS01299; EPHRN.1.
 CC 3D-structure; Developmental protein; Differentiation; Glycoprotein;
 CC Neurogenesis; Phosphorylation; Signal; Transmembrane.
 CC SIGNAL 1 28
 CC CHAIN 29 336
 CC TOPO_DOM 29 232
 CC TRANSMEM 23 253
 CC TOPO_DOM 254 336
 CC MOTIF 334 336
 CC PDZ recognition motif (Potential).

FT CARBOHYD 39 39 N-linked (GlcNAc...)
 FT CARBOHYD 142 142 N-linked (GlcNAc...)
 FT DISULFID 65 104
 FT DISULFID 92 156
 FT CONFLICT 3 4 Missing (in Ref. 3).
 FT CONFLICT 177 177 A -> T (in Ref. 1).
 FT STRAND 36 37
 FT TURN 40 41
 FT TURN 43 44
 FT STRAND 46 46
 FT TURN 47 49
 FT STRAND 50 52
 FT TURN 57 58
 FT STRAND 60 65
 FT TURN 72 73
 FT STRAND 79 84
 FT TURN 86 90
 FT TURN 91 92
 FT STRAND 93 93
 FT STRAND 99 104
 FT TURN 107 108
 FT STRAND 111 116
 FT TURN 124 125
 FT STRAND 131 132
 FT STRAND 134 139
 FT TURN 145 147
 FT HELIX 148 149
 FT STRAND 152 152
 FT TURN 154 154
 FT HELIX 155 158
 FT STRAND 162 166
 SQ SEQUENCE 336 AA; 37202 MW; D0889496B399554 CRC64;

Query Match 25.7%; Score 628.5; DB 1; Length 336;
 Best Local Similarity 41.8%; Pred. No. 1.4e-32;
 Matches 137; Conservative 49; Mismatches 129; Indels 13; Gaps 5;

QY 14 GALLLGLVGLVSGLSLEPVNNSANKRPOAEGVLYLPQIGDRDLDCPRARPPGPHSS 73
 DB 17 GLLMVLCRTAISRLSVLEPYNNSNSKFLPGQGLVLYPQIGDKDILCPKV--DSKTV 73
 QY 74 PNYEFYKLYLVGAQGRCEAPPAAPMLLTCDRPLDLFTTKFQESYENLNGHERSHH 133
 DB 74 GQYEVYKYVMVDKQDRCCTIKKENTPLNLCARPDDVAFITKFOESFENLNGLEFQKK 133
 QY 134 DYIIATSDGTREGLESIGGVCLTRGMKVLRLVGO--SPRGAVPRKPVSEMPER-DR 190
 DB 134 DYIIISTNSGLELDNOEGVQCOTRAMKILMKVGQDASASARNGPTRRPELEAGTN 193
 QY 191 GAHSLPEKKNLPQDPTSNATSRGAEGLPPSPMPAVAGAAGLALLLLGVAAGAGAMC 250
 DB 194 GRSSTSPVKXNPFGSGSTDGNSAGHSNNLLGSEVALFPGIISGCTIFVIIITLVVLL 253
 QY 251 WRRRAKPEESRHPGSGFRGSGSLGLGGGGMGPRAEPBELGIALRGGAADPFCFH 310
 DB 254 KYRRRRKRSPOHTTLLSLTSLATPRKGGNN---NGSEPSVITPLR---TADSVFCFH 306
 QY 311 YEKVSGDYGHPIYIVODGPPQSPNNIYY 338
 DB 307 YEKVSGDYGHPIYIVODGPPQSPNNIYY 334

RESULT 8
 Q4FJM3_MOUSE PRELIMINARY; PRT; 336 AA.
 ID Q4FJM3_MOUSE PRELIMINARY; PRT; 336 AA.
 AC Q4FJM3;
 DT 13-SEP-2005 (T-EMBLrel. 31, Created)
 DT 13-SEP-2005 (T-EMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (T-EMBLrel. 31, Last annotation update)
 DE Efn2 protein.
 GN Name=Efn2;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muroidea; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Ebert J., Muenstermann E., Schatten R., Henze S., Bohn E.,
 RA Mollenhauer J., Wiemann S., Schick M., Korn B.,
 RT "Cloning of mouse full open reading frames in Gateway(R) system entry
 RT vector (pDONR201).";
 RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; CT010381; CAJ18588.1; -; mRNA.
 SQ SEQUENCE 336 AA; 37202 MW; D0889496B399554 CRC64;

Query Match 25.7%; Score 628.5; DB 2; Length 336;
 Best Local Similarity 41.8%; Pred. No. 1.4e-32;
 Matches 137; Conservative 49; Mismatches 129; Indels 13; Gaps 5;

QY 14 GALLLGLVGLVSGLSLEPVNNSANKRPOAEGVLYLPQIGDRDLDCPRARPPGPHSS 73
 DB 17 GLLMVLCRTAISRLSVLEPYNNSNSKFLPGQGLVLYPQIGDKDILCPKV--DSKTV 73
 QY 74 PNYEFYKLYLVGAQGRCEAPPAAPMLLTCDRPLDLFTTKFQESYENLNGHERSHH 133
 DB 74 GQYEVYKYVMVDKQDRCCTIKKENTPLNLCARPDDVAFITKFOESFENLNGLEFQKK 133
 QY 134 DYIIATSDGTREGLESIGGVCLTRGMKVLRLVGO--SPRGAVPRKPVSEMPER-DR 190
 DB 134 DYIIISTNSGLELDNOEGVQCOTRAMKILMKVGQDASASARNGPTRRPELEAGTN 193
 QY 191 GAHSLPEKKNLPQDPTSNATSRGAEGLPPSPMPAVAGAAGLALLLLGVAAGAGAMC 250
 DB 194 GRSSTSPVKXNPFGSGSTDGNSAGHSNNLLGSEVALFPGIISGCTIFVIIITLVVLL 253
 QY 251 WRRRAKPEESRHPGSGFRGSGSLGLGGGGMGPRAEPBELGIALRGGAADPFCFH 310
 DB 254 KYRRRRKRSPOHTTLLSLTSLATPRKGGNN---NGSEPSVITPLR---TADSVFCFH 306
 QY 311 YEKVSGDYGHPIYIVODGPPQSPNNIYY 338
 DB 307 YEKVSGDYGHPIYIVODGPPQSPNNIYY 334

RESULT 9
 EFN2_HUMAN STANDARD; PRT; 346 AA.
 ID EFN2_HUMAN
 AC P98172;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Ephrin-B1 precursor (EPH-related receptor tyrosine kinase ligand 2)
 DE (LEK-2) (Euk ligand) (Euk-L).
 GN Name=EFNB1; Synonyms=EFL-3, EPLG2, LEK2;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Eukaryota; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
 OC Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Placenta;
 RX MEDLINE=94349923; PubMed=8070404;
 RA Beckmann M.P., Cerretti D.P., Baum P., Vanden Bos T., James L.,
 RA Farran T., Kozlosky C., Hollingsworth T., Shilling H., Maraskovsky E.,
 RA Fletcher F.A., Hlochak V., Pawson T., Lyman S.D.,
 RT "Molecular characterization of a family of ligands for eph-related
 RT tyrosine kinase receptors.";
 RL EMBO J. 13:3757-3762(1994).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=95063919; PubMed=7973638;
 RA Davis S., Gale N.W., Aldrich T.H., Maisonnier P.C., Hlochak V.,
 RA Pawson T., Goldfarb M., Yancopoulos G.D.,
 RT "Ligands for EPH-related receptor tyrosine kinases that require

RT membrane attachment or clustering for activity.";
RL Science 266:816-819(1994).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Fletcher P.A., Huebner K., Shaffer L.G., Monaco A., Mueller U.,
RA Kozlovsky C., Druck T., Simoneaux D.K., Fairweather N., Chelly J.,
RA Cerretti D.P., Belmont J.W., Beckmann M.P., Lymn S.D.;
RT "Assignment of the human Elk1 ligand gene, EPLG3, to chromosome region
Xq12.";
RT Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15772651; DOI=10.1038/nature03440;
RA Rose M.T., Gieffah D.V., Coffey A.J., Scherer S., McLeay K., Muzny D.,
RA Plazer M., Howell G.R., Burrows C., Bird C.P., Frankish A.,
RA Lovell F.L., Howe K.L., Ashurst J.L., Fulton R.S., Sudbrak R., Wen G.,
RA Jones M.C., Hurler M.E., Andrews T.D., Scott C.E., Seabrook R.,
RA Ramey J., Whitaker A., Deadman R., Carter N.P., Hunt S.E., Chen R.,
RA Cree A., Gunaratne P., Havlak P., Hodgson A., Metzker M.L.,
RA Richards S., Scott G., Steffen D., Sodergren E., Wheeler D.A.,
RA Worley K.C., Ainscough R., Ambrose K.D., Ansari-Lari M.A., Arachya S.,
RA Ashwell R.I., Babbage A.K., Bagdley C.L., Ballibio A., Banerjee R.,
RA Barter G.E., Barlow K.F., Barrett I.P., Bates K.N., Beare D.M.,
RA Beasley H., Beasley O., Beck A., Bethel G., Blechschmidt K., Brady N.,
RA Bray-Allen S., Bridgeman A.M., Brown A.J., Brown M.J., Bonnin D.,
RA Brutford E.A., Buhay C., Burch P., Burford D., Burgess J., Burrill W.,
RA Burton J., Bye J.M., Carder C., Carrel L., Chako J., Chapman J.C.,
RA Chavez D., Chen E., Chen G., Chen Y., Chen Z., Chnault C.,
RA Ciccodicola A., Clark S.Y., Clarke G., Clee C.M., Clegg S.,
RA Clerc-Blanchet K., Clifford K., Copley V., Cole C.G., Conger J.S.,
RA Corby N., Connor R.E., David R., Davies J., Davis C., Davis J.,
RA Delgado O., Deshazo D., Dhami P., Ding Y., Dinh H., Dodsworth S.,
RA Draper H., Dugan-Rocha S., Dunham A., Dunn M., Durbin K.J., Dutta I.,
RA Bades T., Ellwood M., Emery-Cohen A., Errington H., Evans K.L.,
RA Faulkner L., Francis F., Frankland J., Fraser A.E., Galoczzy P.,
RA Gilbert J., Gill R., Gloeckner G., Gregory S.G., Gribble S.,
RA Griffiths C., Grocock R., Gu Y., Gwilliam R., Hamilton C., Hart E.A.,
RA Hawes A., Heath P.D., Heltmann K., Hennig S., Hernandez J.,
RA Hinemann B., Ho S., Hoffe M., Howden P.J., Huckle E.J., Hume J.,
RA Hunt P.J., Hunt A.R., Isherwood J., Jacob L., Johnson D., Jones S.,
RA de Jong P.J., Joseph S.S., Keenan S., Kelly S., Kershaw J.K., Khan Z.,
RA Kiochs P., Klages S., Knights A.J., Kosiura A., Kovat-Smith C.,
RA Laid G.K., Langford C., Lawlor S., Leversha M., Lewis L., Liu W.,
RA Lloyd C., Lloyd D.M., Louisess G., Loveland J.E., Lovell J.D.,
RA Lozdo R., Lu J., Lyne R., Ma J., Maheshwari M., Matthews L.H.,
RA McDowell J., McLaren S., McMurray A., Meidl P., Mettlinger T.,
RA Milne S., Miner G., Mistry S.L., Morgan M., Morris S., Mueller I.,
RA Mullikin J.C., Nguyen N., Nordstiek G., Nyakatura G., O'dell C.N.,
RA Okunou G., Palmer S., Pandian R., Parker D., Parrish J.,
RA Pasternak S., Patel D., Pearce A.V., Pearson D.M., Pelan S.E.,
RA Perez L., Porter K.M., Ramsey Y., Reichwald K., Rhodes S.,
RA Ridler K.A., Schlesinger D., Schueler M.G., Sehra H.K.,
RA Shaw-Smith C., Shen H., Sheridan E.M., Showkneen R., Shuce C.D.,
RA Smith W.L., Sothman B.C., Steingraber H.B., Steward C.A., Storey R.,
RA Swann R.M., Swarbrick D., Taber P.E., Taudien S., Taylor T.,
RA Teague B., Thomas K., Thorpe A., Tims K., Tracey A., Trevanton S.,
RA Tromans A.C., d'Urso M., Verdusco D., Villaseca D., Waldron L.,
RA Wall M., Wang Q., Warren J., Warr J.G., Wei X., West A.,
RA Whitehead S.L., Whiteley M.N., Wilkinson J.E., Willey D.L.,
RA Woodmansey R.L., Wray P.W., Yen J., Zhang J., Zhou J., Zoghbi H.,
RA Zorilla S., Buck D., Reinhardt R., Poustka A., Rosenthal A.,
RA Lebrach S., Meindl A., Minx P.J., Hillier L.W., Willard H.F.,
RA Wilson R.K., Waterston R.H., Rice C.M., Vaudin M., Coulson A.,
RA Nelson D.L., Weinstein G., Sulston J.E., Durbin R., Hubbard T.,
RA Gibbs R.A., Beck S., Rogers J., Bentley D.R.;
RT "The DNA sequence of the human X chromosome.";
RL Nature 434:325-337(2005).
RN [5]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Eye, and Skin,
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan K.J., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stalderon M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carinci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullish S.J.,
RA Bosak S.A., McKean P.J., McKernan K.J., Malek A.C., Gunaratne P.H.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fabhey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmitz J., Myers R.M.,
RA Rottierfeld Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [6]
RP PROTEIN SEQUENCE OF 28-42.
RX PubMed=15340161; DOI=10.1110/ps.04682504;
RA Zhang Z., Henzel W.J.;
RT "Signal peptide prediction based on analysis of experimentally
RT verified cleavage sites.";
RL Protein Sci. 13:2819-2824(2004).
RN [7]
RP INTERACTIONS WITH GRIP1 AND GRIP2.
RC TISSUE=Fetal brain;
RX MEDLINE=99211388; PubMed=10197531; DOI=10.1016/S0896-6273(00)80706-0;
RA Brueckner K., Pablo Labrador J., Scheffele P., Hebd A., Seeburg P.H.,
RA Klein R.;
RT "EphrinB ligands recruit GRIP family PDZ adaptor proteins into raft
RT membrane microdomains.";
RL Neuron 22:511-524(1999).
RN [8]
RP VARIANTS CENS LBU-54 AND IIE-111.
RX PubMed=15124102; DOI=10.1086/421532;
RA Wieland I., Jakubiczka S., Muschke P., Cohen M., Thiele H.,
RA Gerlach K.L., Adams R.H., Miescher P.;
RT "Mutations of the ephrin-B1 gene cause craniofrontonasal syndrome.";
RL Am. J. Hum. Genet. 74:1209-1215(2004).
RN [9]
RP VARIANTS CENS THR-62, SER-98, PRO-115, HIS-119, THR-119, SER-151;
RP VAL-151, PRO-155, IIE-158 AND VAL-158, AND VARIANT HIS-154.
RX PubMed=15166289; DOI=10.1073/pnas.0402819101;
RA Twigg S.R.F., Kan R., Babbs C., Bochkova E.G., Robertson S.P.,
RA Wall S.A., Morris-Kay G.M., Wilkie A.O.M.;
RT "Mutations of ephrin-B1 (EFNB1), a marker of tissue boundary
RT formation, cause craniofrontonasal syndrome.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:8652-8657(2004).
RN [10]
RP VARIANTS CENS ARG-27, LBU-54; SER-119, HIS-119; ALA-137; PHE-138;
RP SER-151; SER-153; TYR-153 AND ARG-182.
RX PubMed=15959873; DOI=10.1002/humu.20193;
RA Wieland I., Reardon W., Jakubiczka S., Franco B., Krese W.,
RA Vincent-DeJorne C., Thierly P., Edwards M., Koenig R., Rusu C.,
RA Schweiger S., Thompson E., Tinschert S., Stewart F., Miescher P.;
RT "Twenty-six novel EFNB1 mutations in familial and sporadic
RT craniofrontonasal syndrome (CFNS).";
RL Hum. Mutat. 26:1-6(2005).
RN [11]
RP FUNCTION: Binds to the receptor tyrosine kinases EphA1 and EphA2.
CC Binds to, and induce the collapse of, commissural axons/growth
CC cones in vitro. May play a role in constraining the orientation of
CC longitudinally projecting axons (By similarity).
CC - SUBUNIT: Interacts with GRIP1 and GRIP2.
CC - SUBCELLULAR LOCATION: Type I membrane protein.
CC - TISSUE SPECIFICITY: Heart, placenta, lung, liver, skeletal muscle,
CC kidney, pancreas.
CC - INDUCTION: By TNF-alpha.
CC - PTM: Inducible phosphorylation of tyrosine residues in the
CC cytoplasmic domain (By similarity).
CC - DISEASE: Defects in EFNB1 are a cause of craniofrontonasal

DR EMBL; BC069342; AAH69342.1; -, mRNA.
DR EMBL; BC074856; AAH74856.1; -, mRNA.
DR EMBL; BC074857; AAH74857.1; -, mRNA.
DR PIR; I84743; I84743.
DR HSSP; P52800; I1KO.
DR SMR; P52799; 27-167.
DR Ensembl; ENSG0000012526; Homo sapiens.
DR HGNC; HGNC:3227; EPNB2.
DR MIM; 600527; -.
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0005886; C:plasma membrane; TAS.
DR GO; GO:0046875; E:ephrin receptor binding; TAS.
DR GO; GO:0007267; P:cell-cell signaling; TAS.
DR GO; GO:0009653; P:morphogenesis; TAS.
DR InterPro; IPR001799; Ephrin.
DR Pfam; PF00812; Ephrin; 1.
DR PRINTS; PR01347; EPHRIN.
DR ProDom; PD002533; EPHRIN; 1.
DR PROSITE; PS01299; EPHRIN; 1.
DR Developmental Protein; Differentiation; Neurogenesis;
KM Phosphorylation; Signal; Transmembrane.
FT SIGNAL 1 27 Potential.
FT CHAIN 28 333 Ephrin-B2.
FT TOPO_DOM 28 229 Extracellular (Potential).
FT TRANSMEM 230 250 Potential.
FT TOPO_DOM 251 333 Cytoplasmic (Potential).
FT MOTIF 331 333 PDZ recognition motif (Potential).
FT CARBOHYD 36 36 N-linked (GlcNAc..?) (Potential).
FT CARBOHYD 139 139 N-linked (GlcNAc..?) (Potential).
FT DISULFID 62 101 By similarity.
FT DISULFID 89 153 By similarity.
SQ SEQUENCE 333 AA; 36923 MW; 6D9932A632626A6A CRC64;

Query Match 25.3%; Score 620.5; DB 1; Length 333;
Best Local Similarity 40.5%; Pred. No. 4,4e-32;
Matches 133; Conservative 52; Mismatches 130; Indels 13; Gaps 5;
QY 14 GALLLLGVLGSLGSLPEPVYVNSANKRFOAEGVLYLPQIGRLDLCRRARPPGPHSS 73
DB 14 GVLMLVLCRAIAKSIYLEPIYVNSNSKFLPGQGLVLYPQIGDKLDICPKV---DSKTV 70
QY 74 PNYEFKLYLVGAAGRCRCEAPPANLLITCDRPDLRFTIKFOEYSPNLMGHEFRSH 133
DB 71 GQYEVYKVMVVDKQADRCTIKCENTPLINCAPDODIKFTIKFOEFSPLNMGLEFQKN 130
QY 134 DVIITATSDGTREGSLGSGVCLTRGMKYLVRVQ--SPRGAVPRKPVSEMPMER-DR 190
DB 131 DVIITATSDGTREGSLGSGVCLTRGMKYLVRVQ--SPRGAVPRKPVSEMPMER-DR 190
QY 191 GAHSLPEKENTLPGDPTSNATSRGAEGPLPPSPMAVAGAGLALLLGVAGAGAMC 250
DB 191 GRSSTSPVKPNPFGSSTDGNSAGSNNILGSEVALFPAIAGSCIIFFIITLVVLL 250
QY 251 WRRRAKPSERHPGSGFSGSLGSGGGMCPREAEGLIALRGGAADPPFCRH 310
DB 251 KYRRRRHKSPHPTTTLSTLATPKRSNN---NGSEPSDIIIPLR--TADSVFCRH 303
QY 311 YEKVSGDYGHPIYIVODGPPSPENITY 338
DB 304 YEKVSGDYGHPIYIVODGPPSPENITY 331

RESULT 11
OSUSV56 HUMAN
ID OSU56_HUMAN PRELIMINARY; PRT; 333 AA.
AC OSU56;
DT 10-MAY-2005 (Tremblrel. 30, Created)
DT 10-MAY-2005 (Tremblrel. 30, Last sequence update)
DT 10-MAY-2005 (Tremblrel. 30, Last annotation update)
DE Ephrin-B2 (Fragment)
GN Name=EPNB2; ORNames=RP11-272L14.1-001;
OS Homo sapiens (human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Dunn M.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ database.
DR EMBL; AL136889; CA13907.1; -, Genomic DNA.
DR GO; GO:0016020; C:membrane; IEA.
FT NON TER 333 333
SQ SEQUENCE 333 AA; 36923 MW; 6D9932A632626A6A CRC64;

Query Match 25.3%; Score 620.5; DB 2; Length 333;
Best Local Similarity 40.5%; Pred. No. 4,4e-32;
Matches 133; Conservative 52; Mismatches 130; Indels 13; Gaps 5;
QY 14 GALLLLGVLGSLGSLPEPVYVNSANKRFOAEGVLYLPQIGRLDLCRRARPPGPHSS 73
DB 14 GVLMLVLCRAIAKSIYLEPIYVNSNSKFLPGQGLVLYPQIGDKLDICPKV---DSKTV 70
QY 74 PNYEFKLYLVGAAGRCRCEAPPANLLITCDRPDLRFTIKFOEYSPNLMGHEFRSH 133
DB 71 GQYEVYKVMVVDKQADRCTIKCENTPLINCAPDODIKFTIKFOEFSPLNMGLEFQKN 130
QY 134 DVIITATSDGTREGSLGSGVCLTRGMKYLVRVQ--SPRGAVPRKPVSEMPMER-DR 190
DB 131 DVIITATSDGTREGSLGSGVCLTRGMKYLVRVQ--SPRGAVPRKPVSEMPMER-DR 190
QY 191 GAHSLPEKENTLPGDPTSNATSRGAEGPLPPSPMAVAGAGLALLLGVAGAGAMC 250
DB 191 GRSSTSPVKPNPFGSSTDGNSAGSNNILGSEVALFPAIAGSCIIFFIITLVVLL 250
QY 251 WRRRAKPSERHPGSGFSGSLGSGGGMCPREAEGLIALRGGAADPPFCRH 310
DB 251 KYRRRRHKSPHPTTTLSTLATPKRSNN---NGSEPSDIIIPLR--TADSVFCRH 303
QY 311 YEKVSGDYGHPIYIVODGPPSPENITY 338
DB 304 YEKVSGDYGHPIYIVODGPPSPENITY 331

RESULT 12
ID OSU56_CHICK PRELIMINARY; PRT; 333 AA.
AC OSU56;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Ephrin-B2 precursor.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Menzel P.; Paegle E.B.;
RT "Coding sequence of chicken ephrin-B2."
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ database.
DR EMBL; AF180729; AAD53948.1; -, mRNA.
DR HSSP; P52800; I1KO.
DR SMR; OSU56; 29-169.
DR Ensembl; ENSGALG0000016856; Gallus gallus.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR001799; Ephrin.
DR Pfam; PF00812; Ephrin; 1.
DR PRINTS; PR01347; EPHRIN.
DR ProDom; PD002533; EPHRIN; 1.
DR PROSITE; PS01299; EPHRIN; 1.
KM Signal.
FT SIGNAL 1 27 Potential.
FT CHAIN 28 333 Ephrin-B2.
SQ SEQUENCE 333 AA; 36761 MW; 4C28E8CB211B7783 CRC64;

Query Match	25.3%	Score 620.5	DB 2:	Length 333
Best Local Similarity	40.2%	Pred. No. 4.4e-32		
Matches	133	Conservative	52	Mismatches 125; Indels 21; Gaps 6
Qy	14	GALLLLGLVGLVSGSLSPVYWNSSANKRFOAGGVLYLPQIGDRDLDCPRARPPRHSS	73	
Db	16	GALVMTALAKSLIVLDPIYWNSSNPKFVLPQGLVLPQIGDKDIIICPKV---	DSKTV 72	
Qy	74	PNVEFYKLYLVGAAGRRCEAPRANLLITCDRPLDLRFITKPFQYSPNLMGNHFRSH	133	
Db	73	GQVEYKKYMWYDKQADSCAIRKDNTPRLNCAKPPQDVKFTTKCFEFPNLMGLFQXK	132	
Qy	134	DYIIATSDGREGLESLOGGVCITRGKMKVLLRVGSGPRGAVPRKPVSEMMER----	188	
Db	133	DYVISTNGSLGELNMGEGVCQTKTKYKMLKVQDPSAGLR---STDPTKRPDEOA	189	
Qy	189	-DRGAHSLREPKENTPGDPTSNATSRGABGLPPSPRPAVAGAAGLALLLLVYAGAG	247	
Db	190	GTNCKSSSTPSFVVDHSGSSTDG--SKAGHSLIGSEVALFAGIASGCIIFVILTVV	247	
Qy	248	AMCRRRRRAKSESNNRPGSGFGSGISGLGGGGMGRPEARPGSLGIALRGGAADPF	307	
Db	248	LLLKYYRRHRKHSPOHTTLLSLSTLATKRGNN---NGSPPSDIIPLR---YADSVF	300	
Qy	308	CPHYEKVSGDYGHPIYIVODGPPSPPIY	338	
Db	301	CPHYEKVSGDYGHPIYIVQEMPPSPPIY	331	

ID	EMBL CHICK	STANDARD	PRT	334 AA.
AC	073612			
DT	15-JUL-1999	(Rel. 38, Created)		
DT	15-JUL-1999	(Rel. 38, Last sequence update)		
DT	10-MAY-2005	(Rel. 47, Last annotation update)		
DE	Ephrin-B1 precursor (CEK5 ligand) (CBL5-L).			
GN	Name=EFNB1			
OS	Gallus gallus (Chicken).			
OC	Eukaryota; Metazoa; Chordata; Vertebrate; Euteleostomi;			
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;			
OC	Gallus.			
OX	NCBI_TaxId=9031;			
OX	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RX	MEDLINE=9723524; PubMed=9070326; DOI=10.1006/dbio.1996.8496;			
RA	Holash J.A., Soans C., Chong L.D., Shao H., Dixit V.M., Pasquale E.B.;			
RT	"Receptor expression of the Eph receptor Ceks and its ligand(s) in			
RT	the early retina.";			
RL	Dev. Biol. 182:256-269(1997).			
CC	-1- SUBUNIT: Binds to the receptor tyrosine kinase EphB2. Interacts			
CC	with GRIP1 and GRIP2 (By similarity).			
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein.			
CC	-1- PPM: Inducible phosphorylation of tyrosine residues in the			
CC	cytoplasmic domain (By similarity).			
CC	-1- SIMILARITY: Belongs to the ephrin family.			
CC	-----			
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use as long as its content is in no way modified and this statement is not			
CC	removed.			
CC	-----			
DR	EMBL, U72394; AAC07986.1; -, mRNA.			
DR	HSSP, P52800; IIKO.			
DR	InterPro; IPR001799; Ephrin.			
DR	Pfam; PF00812; Ephrin, 1.			
DR	PRINTS; PR01347; EPHRIN.			
DR	ProDom; PD002533; Ephrin; 1.			
DR	PROSITE, PS01299; EPHRIN; 1.			
KW	Developmental protein; Differentiation; Glycoprotein; Neurogenesis;			
KW	Phosphorylation; Signal; Transmembrane.			

FT	SIGNAL	1	25	Potential.
FT	CHAIN	26	334	Ephrin-B1.
FT	TOPO_DOM	26	231	Extracellular (Potential).
FT	TRANSMEM	232	252	Potential.
FT	TOPO_DOM	253	334	Cytoplasmic (Potential).
FT	MOTIF	332	334	PDZ recognition motif (Potential).
FT	CARBOHYD	135	135	N-linked (GlcNAc. .) (Potential).
FT	DISULFID	60	97	By similarity.
FT	DISULFID	85	149	By similarity.
SO	SEQUENCE	334 AA;	36859 MW;	48AF556BED56CD5 CRC64;

Query Match	25.3%	Score 619;	DB 1;	Length 334;
Best Local Similarity	39.3%	Pred. No. 5.6e-32;		
Matches 144;	Conservative 50;	Mismatches 100;	Indels 72;	Gaps 13

```

QY      PGGVR--VEATLLLLGLVLGVLSELEPYMNSANKRFOAEQGVYLYPOIGDRLDLCFPA 65
Db      4  PRGGRULLGVLLALCRILAAPLAKSLERPSWAGNPKFMGSGGLVYIYEIGDKDIDICPKA 63
QY      66  RPPGPHSSPNVEYXYLYLVGGAQGRCEAPAPNILLTCRPRDULRFTIKFOEYSBNLW 125
Db      64  EPSEKP-----YDYLYKLIVLKQDQADAGSTWMDPNVLVYTCNRPEGEINFITKFOGFSBNYM 118
QY      126  GHEFRSHNDYIILATSDGTRBGLSELOQGVCLTGMKVLLRVLGQSPRGGAVPKRPVSEMP 185
Db      119  GLEFRKQDDYFTITSNGTLDGLERREGVOCOTSRMKIWMKVGGDP--NAVIPGLTTSRP 177
QY      186  MER-----DRGAHSL----BPGKNLPGDPTLSNA--TSRGAEGRLPPSPMAPAVA 231
Db      178  SKEDNTVTKIYIQSFRHKVPTVEBPK--PGSYNQNGOETGCPSPDGL--SKVAIVFAA 232
QY      232  AGS-----LATLLGLVAGAGAMCWRRAKRPSESRH-----PGGSPGRC 272
Db      233  IGAGCVIFILIIIFLVLLIKI-----RKHNRHGTQGRALALSLSTLAPKCSGNA 283
QY      273  GSLGLGCGGGMGRERAEFGELGIALRGGAADPRPCHYEKNVSGDYGHPIYIYIQDGRPOS 332
Db      284  GS-----EPSSDIILPIR--TTENNYCPHYEKVSGDYGHPIYIYIQDGRPOS 366
QY      333  PPIIYX 338
Db      327  PANIYY 332

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RESULT 14	EFNB2_BRARE	STANDARD;	PRT;	332 AA.
EFNB2_BRARE				
ID	EFNB2_BRARE	STANDARD;	PRT;	332 AA.
AC	073874;			
DT	15-JUL-1999 (Rel. 38, Created)			
DT	15-JUL-1999 (Rel. 38, Last sequence update)			
DT	10-MAY-2005 (Rel. 47, Last annotation update)			
DE	Ephrin-B2a precursor.			
GN	Name=efnb2a; Synonyms=efnb2;			
OS	Brachydanio rerio (Zebrafish).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;			
OC	Cyprinidae; Danio.			
OX	NCBI_TaxId=7955;			
RN				
UN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RP	MEDLINE=98438455; PubMed=9765210;			
RA	Durbain L., Brennan C., Shiom K., Cooke J., Barrios A.,			
RA	Shannugalingam S., Guthrie B., Lindberg R., Holder N.,			
RT	"epb signaling is required for segmentation and differentiation of the			
RT	somites.";			
RL	Genes Dev. 12:3096-3109(1998).			
RN	[2]			
RN	NUCLEOTIDE SEQUENCE.			
RP	MEDLINE=21590837; PubMed=11397014; DOI=10.1006/dbio.2001.0281;			
RA	Chan J., Mobly J.D., Serluca F.C., Chen J.N., Goldstein N.B.,			
RA	Thomas M.C., Cleary J.A., Brennan C., Fishman M.C., Roberts T.M.,			
RT	"Morphogenesis of prechordal plate and notochord requires intact			
RT	epb/ephrin b signaling.";			

251 WRRRAKPSRRHGGSGFGRGSLGLGGGCGKGPPEAPPGELIALRGGAADPPFCPH 310
251 KRRRRRRKRSPOHTTLSTLSTLATPRSGNN-----NGSPSPDIIPLR---TADSVFCPH 303
QY 311 YEKVSGDYGHPPYIVODGPPGSPNNIYY 338
DB 304 YEKVSGDYGHPPYIVQEMPPGSPNNIYY 331

RESULT 2

US-10-949-720-390
Sequence 390, Application US/10949720
Publication No. US20050249736A1
GENERAL INFORMATION:
APPLICANT: Krasnoperov, Valery
APPLICANT: Zozulya, Sergey
APPLICANT: Kertes, Nathalie
APPLICANT: Reddy, Ramachandra
APPLICANT: Gili, Parkash
TITLE OF INVENTION: POLYPEPTIDE COMPOUNDS FOR INHIBITING
FILE REFERENCE: VASG-P02-002
CURRENT APPLICATION NUMBER: US/10/949,720
PRIOR FILING DATE: 2004-09-23
PRIOR APPLICATION NUMBER: US 60/454,432
PRIOR FILING DATE: 2003-03-12
PRIOR APPLICATION NUMBER: US 60/454,300
PRIOR FILING DATE: 2003-03-12
PRIOR APPLICATION NUMBER: US 10/800,350
PRIOR FILING DATE: 2004-03-12
NUMBER OF SEQ ID NOS: 425
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 390
LENGTH: 459
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Recombinant B2EC-FC protein
US-10-949-720-390

Query Match 18.4%; Score 451.5; DB 6; Length 459;

Best Local Similarity 29.5%; Pred. No. 3.3e-29;
Matches 122; Conservative 47; Mismatches 115; Indels 129; Gaps 11;

QY 14 GALLLLGVGLVSGLSLEPYVWNSANKRFOAGGVLYVPOIGDRLDLCPRARPPGPHSS 73
DB 14 GLLMLCRLTAISGLVLEPIYWNSSSKFLPGQGLVLYVPOIGDKDIIICPKV---DSKTV 70
QY 74 PNYEFYKLYLVGAQGRCEAPAPNLLITCDRPLDLRFTIKFOEYSPNLWGHEFRSHH 133
DB 71 GQYEVYKVMVDKQADRCTIKENTPLINCAPDQDIKFTIKFOEYSPNLWGHEFRSHH 130
QY 134 DYIIITSDGTREGLESLOGVCLTRGMKVLLRVGQSPRGAVPRKPVSEMPNERDGA 193
DB 131 DYIIISTSGSLGDLNQGVCQTRAMKILMKVQ----- 166
QY 194 HSLPEKENTLPDPTSNATSRGAEGLPPSPMPAVAGAAGLALLLLGVAAGAMCMRR 253
DB 167 -----DASSAGSTRNKDPTRRPEL-----AGTNG----- 191
QY 254 RRAKPSRRHGGSGFGRGSLGLGGGCGMPPEAPPGELIALRGGAADP----- 305
DB 192 RSTTSPFYKPNPSSSTDGNSAGHSGNNILG-SEVDP-----EPKSCDKTHT 237
QY 306 -PPCPHYEVKVS-----DYGH-----PY 323
DB 238 CPCCPAPPELLGGSVFLPPPKPDITLMISRTPEVTCVVVDVSHEDDEVKFMVVDGEVH 297
QY 324 IVODGPPSPNNIYYTSISVLEWPIHLTIQLFMRSGKSVTFTLPPVOVIT 376
DB 298 NAKTKREQINSTYIVVSVL--TVLHQMWNKEKYK--KVSXKALPAPIEKT 347

RESULT 3

US-10-949-720-388
Sequence 388, Application US/10949720
Publication No. US20050249736A1
GENERAL INFORMATION:
APPLICANT: Krasnoperov, Valery
APPLICANT: Zozulya, Sergey
APPLICANT: Kertes, Nathalie
APPLICANT: Reddy, Ramachandra
APPLICANT: Gili, Parkash
TITLE OF INVENTION: POLYPEPTIDE COMPOUNDS FOR INHIBITING
FILE REFERENCE: VASG-P02-002
CURRENT APPLICATION NUMBER: US/10/949,720
PRIOR FILING DATE: 2004-09-23
PRIOR APPLICATION NUMBER: US 60/454,432
PRIOR FILING DATE: 2003-03-12
PRIOR APPLICATION NUMBER: US 60/454,300
PRIOR FILING DATE: 2003-03-12
PRIOR APPLICATION NUMBER: US 10/800,350
PRIOR FILING DATE: 2004-03-12
NUMBER OF SEQ ID NOS: 425
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 388
LENGTH: 233
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Recombinant B2EC protein
US-10-949-720-388

Query Match 18.0%; Score 442; DB 6; Length 233;
Best Local Similarity 35.8%; Pred. No. 8.7e-29;
Matches 97; Conservative 36; Mismatches 76; Indels 62; Gaps 4;

QY 14 GALLLLGVGLVSGLSLEPYVWNSANKRFOAGGVLYVPOIGDRLDLCPRARPPGPHSS 73
DB 14 GLLMLCRLTAISGLVLEPIYWNSSSKFLPGQGLVLYVPOIGDKDIIICPKV---DSKTV 70
QY 74 PNYEFYKLYLVGAQGRCEAPAPNLLITCDRPLDLRFTIKFOEYSPNLWGHEFRSHH 133
DB 71 GQYEVYKVMVDKQADRCTIKENTPLINCAPDQDIKFTIKFOEYSPNLWGHEFRSHH 130
QY 134 DYIIITSDGTREGLESLOGVCLTRGMKVLLRVGQSPRGAVPRKPVSEMPNERDGA 193
DB 131 DYIIISTSGSLGDLNQGVCQTRAMKILMKVQ----- 166
QY 194 HSLPEKENTLPDPTSNATSRGAEGLPPSPMPAVAGAAGLALLLLGVAAGAMCMRR 253
DB 167 -----DASSAGSTRNKDPTRRPEL-----AGTNG----- 191
QY 254 RRAKPSRRHGGSGFGRGSLGLGGGCGMG 284
DB 192 RSTTSPFYKPNPSSSTDGNSAGHSGNNILG 222
RESULT 4
US-10-131-826A-288
Sequence 288, Application US/10131826A
Publication No. US20050245730A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvarot, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven

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; APPLICANT: Smith,Victoria
; APPLICANT: Stewart,Timothy A.
; APPLICANT: Tumas,Daniel
; APPLICANT: Watanabe,Colin K
; APPLICANT: Wood,William
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P330R1C128
; CURRENT APPLICATION NUMBER: US/10/131, 826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 288
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-288

Query Match      6.7%, Score 164.5; DB 6; Length 204;
Best Local Similarity 27.7%, Pred. No. 1.2e-06;
Matches 46; Conservative 31; Mismatches 74; Indels 15; Gaps 5;

Qy      18 LGGVGLVSGLSLEPYKMSANKRFOAGGYVYLPQIGRLDLCPRAPRPHSS-PRV 76
Db      8 LGGCCSLAADRHYTFMSSNPKFNE-DYTHVQNLNDYDICHYE---DHSADAM 63
Qy      77 EFKYLYVGAQGRCEAPAPNLLTCDRPLD---DLRFITKFOEYSPNLGHEFRSH 133
Db      64 EGYILVLVHEEYQLQPSKQGVNRPAKHGREKLSKFFQFTFTLGKFKEGH 123
Qy      134 DYIITATSDGTREGLESLOGGVCVLTGMKYLRLVSGSPRGAVPRK 179
Db      124 SYVIISKPIHDEDR-----CLRUKVTVSGKITSPQAHNDFQZ 162

RESULT 5
US-10-220-824-8
; Sequence 8; Application US/10220824
; Publication No. US2005027603A1
; GENERAL INFORMATION:
; APPLICANT: Viewmed Limited
; TITLE OF INVENTION: Compositions for gene therapy of rheumatoid arthritis including a
; FILE REFERENCE: OP0208/PCT
; CURRENT APPLICATION NUMBER: US/10/220, 824
; CURRENT FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: KR 2001-0000691
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Kopatentin 1.71
; SEQ ID NO 8
; LENGTH: 1516
```

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-220-824-8

Query Match      5.9%, Score 144.5; DB 6; Length 1516;
Best Local Similarity 23.5%, Pred. No. 0.00049;
Matches 73; Conservative 18; Mismatches 82; Indels 137; Gaps 15;

Qy      52 PQIGRLDLCPRAPRPHSSPNYEFYLYVGAQGRCEAPAPNLLTCDRPLDL 111
Db      620 PEGVER-----GPRGQGRP-----GPRGSP----- 640
Qy      112 RFTIKFOEYSPNLGHEFRSHDYIITATSDTREG--LESLOGGVCVLTGMKYLRLV 169
Db      641 -----FR--HDKLTFLIDMSSGCGDEALRG----- 665
Qy      170 SPRGAVPRKP--VSEMPERDRGAHSL-IGKENTLQDDPFSNATSRGAEPLPPSP 226
Db      666 -PRGPRPPGPPGVGLPGEPRFGVNSSDVBPAGLPGLPVP-----GREGPPGGLP 717
Qy      227 AVAGAAGLALLLLGVAGAGAMCWRRRRAKSESRRHPGSGFRGSGSLGSGGGMGR 286
Db      718 GPPGPPG-----RSGPRGTGQKSLGEGAGRGHK 749
Qy      287 EAPGELGIALRG-----GAADPPFCP-----HYEYSGDYGHVYIV---Q 326
Db      750 KGAEPGAGRGESGLAAGAPGAPGPPGPPGPPGGLPAGFDMEGS-CCGFWSTARSA 808
Qy      327 DGPQSPPI 336
Db      809 DG-PGPPGL 817

RESULT 6
US-11-186-284-35
; Sequence 35; Application US/11186284
; Publication No. US2005026493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kametkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; FILE REFERENCE: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; CURRENT APPLICATION NUMBER: US/11/186,284
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 1496
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-186-284-35

Query Match      5.8%, Score 142.5; DB 7; Length 1496;
Best Local Similarity 29.1%, Pred. No. 0.0007;
Matches 55; Conservative 15; Mismatches 76; Indels 43; Gaps 9;

Qy      169 QSPRG--GAV--PRKVSSEMPERDRGAHSLERKENTLPG-----DPTSNATSRGAE 217
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Db      500 RGPFGDPECTLCPPGPVGERGAPKRGF-----PSSDGLPGKQAQGBGPVGSSGGRPKSQ 554
Qy      218 GPLPPSPMAVAGAAGGIALLLLVAGAGAMCWMRRRRRAKPSSESRHPPG-----GSFGRGG 273
Db      555 GDPGRPGEPGLPGARG-----LTGNPGVQGBEKGKGLPLGAPGEBDGRPGPPSISIGIKQPG 609
Qy      274 SLGICGGGGMPPREAREPEBELGIALRGGAADPPPCPHXKYSGDYGHVYIVQDGP--- 330
Db      610 TMGLPPGPKSGNDPDKPEAG---NPGVPGQRGAPGKDKGVGPYP---GPGLR 659
Qy      331 -----QSP 334
Db      660 GERGEQGP 668

RESULT 7
US-11-186-284-37
; Sequence 37, Application US/11186284
; Publication No. US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MPW01-029P2RNM
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 744
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-186-284-37

Query Match          5.8%; Score 142; DB 7; Length 744;
Best Local Similarity 23.5%; Pred. No. 0.00034;
Matches 73; Conservative 16; Mismatches 96; Indels 126; Gaps 14;;

Qy      67 PPGHSSBNVEFYKYLIVGAQGRRCAPPAENLLTCDRDPDLRTIKFEQYSPNLMG 126
Db      198 PPGPHGLG-----IGKPGGPELPQGPBK----- 222
Qy      127 HEPHSHDYIIATISDGTREGIESIQGVCILTRGMKULLRVQSPRGGAIVPRKPVSEMPM 186
Db      223 -----GDRPGKGLPGQG-----LRPRKDGKGGMGGAAPGVKGP- 256
Qy      187 ERDRGAHSLPEKKNELPGDPTSNNTS--RGAEGPLPPSPMAVAGAAGLALLLL-----G 241
Db      257 ---PGMHGL-PGPVGLPGVGKPGVITGPPGQGLGKFGAEGEPGRQGPigvPGVQGP 311
Qy      242 VAGAAGAMCWMRRRRRAKPSSESRHPPG-----PGSFRGGS 274
Db      312 IPGIG-----KPGQDGI PQGPGRPGKGEQGLPGLPGAPGLPGIGKRGFPGRKD 361
Qy      275 LGLGG-GGGMGPREAREPEBELGIALRGGAADP--PFCYHEKVSGDYGHVYIVQDGP-- 329

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Db      362  RGMGVPGALGPR-GEKGPICGSPICGSPCBPGLRGIP-----GFMGPALGIPGPKG 414
QY      330  -----PQSP 334
Db      415  EGGIVGPGGPP 425

RESULT 8
US-11-186-284-39
/ Sequence 39, Application US/11186284
/ Publication No. US20050266493A1
/ GENERAL INFORMATION:
/ APPLICANT: Millennium Pharmaceuticals, Inc.
/ APPLICANT: Berger, Allison
/ APPLICANT: Guillemette, Tracy L.
/ APPLICANT: Kamatkar, Shubhangi
/ APPLICANT: Schlegel, Robert
/ APPLICANT: Monahan, John E.
/ APPLICANT: Thibodeau, Stephen N.
/ APPLICANT: Burgart, Lawrence J.
/ TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
/ TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
/ TITLE OF INVENTION: THERAPY OF COLON CANCER
/ FILE REFERENCE: PPM01-029P2RM
/ CURRENT APPLICATION NUMBER: US/11/186, 284
/ CURRENT FILING DATE: 2005-07-21
/ PRIOR APPLICATION NUMBER: US/10/301, 822
/ PRIOR FILING DATE: 2002-11-21
/ PRIOR APPLICATION NUMBER: US 60/339, 971
/ PRIOR FILING DATE: 2001-12-10
/ PRIOR APPLICATION NUMBER: US 60/361, 978
/ PRIOR FILING DATE: 2002-03-05
/ PRIOR APPLICATION NUMBER: US 60/381, 988
/ PRIOR FILING DATE: 2002-05-20
/ NUMBER OF SEQ ID NOS: 228
/ SOFTWARE: FASTSEQ for Windows Version 4.0
/ SEQ ID NO 39
/ LENGTH: 744
/ TYPE: PRT
/ ORGANISM: Homo Sapiens
US-11-186-284-39

Query Match      5.8%; Score 142; DB 7; Length 744;
Best Local Similarity 23.3%; Pred. No. 0.00034;
Matches 72; Conservative 16; Mismatches 99; Indels 122; Gaps 13;

QY      67  PPGHSSPNVEFYLYLVGGAQGRRCAPAPNLLTLCDBPDLRLFTIKFQEYSPNLWG 126
      |||||
      198  PPGHGLPG-----IGKRGGGLGCGQPK----- 222
QY      127  HEFSSHHDYIIATSDTREGLESLOGVCITRGMYLLRVGSPRGGAVERKRVSEMPM 186
      :|||
      223  -----GDRGPKGLPDPG-----LRPKDKDGCMGADGVKCP- 256
Db      187  ERDGAHSLRPGKENTPGDPTSNATRS-RAHEGLPFPSPMAYVAGAAAGLALLL-----G 241
      :|||
      257  ---PGMHG-PPGVEVGLPGVKRPGVTGPPGQGLKRGVAGEBPGQPIGVPGVQGPBG 311
QY      242  VAGAGAMCWRARRAKSESRRHPG-----PGSFGKGS 274
      |||||
      312  IPIG-----KRGQDGIPIQOPRPGGKGQGLGLPGPGLDPIGKRGFPGRPGD 361
QY      275  LGLGG-GGGMGPRAEPGELGIALRGGAADPRPCPHYEKVSGDYGHRYIIVDDGP----- 329
      :|||
      362  RGMGVPGALGPR-GEKGPICGAPIGG---PGEPLGPIPGMGPALGFPQKGE 416
QY      330  ---PQSP 334
Db      417  GIVGPGGPP 425

RESULT 9
US-10-821-234-964

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```
; Sequence 964, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 964
; LENGTH: 1166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-964

Query Match      5.8%; Score 141.5; DB 6; Length 1166;
Best Local Similarity 28.1%; Pred. No. 0.00063;
Matches 59; Conservative 11; Mismatches 83; Indels 57; Gaps 8;

QY 165 LRVGSP-----RGAVPRKP-----VSEMPMER-----DRGAHSLPCK 200
DB 697 LRGGGPRPBGCKGAGGPRGGAGTGTGCGMPERKGLSPGKKGK-----EPGG 751
QY 201 ENLPDPTSNATSGAEGPLPPSPMPAVAGAAG-GLALLLLGVAGAGAMCWRRRRAKPS 259
DB 752 PGADVPGKMDG-PRGPTGTGIGPPGPAQPGDKGEGGAPGLPGIAGPRGSPGSRGGETGPPG 810
QY 260 ESRHRG-----PGSRGSGSLGLGGGCGMKGRREARPGSLGIALRGGA 303
DB 811 PAFGPGAPQNGEPGCKGGRGAPGKKGEGGPPGVAGPPKDGTSGHPIG----- 861
QY 304 DRPPCHYEKVSVDYGHVYIVODGPPQSP 333
DB 862 -PPGPRGNRGERGSESGPHGPPGPPPP 890

RESULT 10
US-11-186-284-33
; Sequence 33, Application US/11186284
; Publication No. US2005026493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhang
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MP001-029P2RM
; CURRENT APPLICATION NUMBER: US/11/186,284
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 1466
```

```
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-186-284-33

Query Match      5.8%; Score 141.5; DB 7; Length 1466;
Best Local Similarity 27.6%; Pred. No. 0.00082;
Matches 61; Conservative 13; Mismatches 74; Indels 73; Gaps 10;

QY 171 PGGAVPRKPVSEMEMERDGA-----AHSLEPKENTLPGDPTSNAT-----SRGAEG 218
DB 844 PPGSSGPAPGPPGQGVKGRGSPGGGAGAFGAGAGLPGPPSSNNGPPGSSPGKDG 903
QY 219 PLPP-----PSMPAVAGAAGL-----ALLLLGVAGAGAMCWRRRRA 256
DB 904 PPGPAGNTGAPGSPGVSGPKDAGQPGKSPGAPGAPGLIAGITGARGLAGPPG 963
QY 257 KPESRHRGP-----GSFRGSGSLGCG-GGCMGP-----REARSELGIAL 297
DB 964 MGPGRGSPGQGVKSGKPGKANGLSGERGPPGGLPGLACTAGEPPGDNPGSDGLPG 1023
QY 298 RCG-----GAADPPCHYEKVSVDYGHVYIVODGPP 330
DB 1024 RUGSPGCKGDKGNGSPGAP-----GAPGP-----GPP 1052

RESULT 11
US-10-821-234-1182
; Sequence 1182, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1182
; LENGTH: 1874
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1182

Query Match      5.6%; Score 137.5; DB 6; Length 1874;
Best Local Similarity 25.5%; Pred. No. 0.0023;
Matches 79; Conservative 15; Mismatches 85; Indels 131; Gaps 18;

QY 61 LCPRARPPGPHSSPNYEFKYLYVGAGAG-----RCEAPPAENLLTCRPPDLD 110
DB 602 LTRGPGVGPSPGS-----GGLGEPGDVGPQGRGVQGPBP-----AGKP--- 642
QY 111 LAFTIKPQESYNNLMGHERSHHDYIATSDGT-----EGLESLOGVVC 156
DB 643 -----GRRGR-----AGSDGAGMPGQGTGPKDRCGVDGAGLPG--- 676
QY 157 LTRGMKVLIRVQSPRGCAVPRKPVSEMEMERDGAHSLBPKENTLPGDPTSNATSRGA 216
DB 677 -----EKGRGDGPGSGPPGPPDDERG--DDGEVGPRLGPEP-----GPRGL 719
QY 217 EGPLPPSPMPAVAGAAGLALLLLGVAGAGAMCWRRRRAKPSRHRG-PSFRGGSGL 275
DB 720 LGPKPBPGRPPGPPGVTG-----MDGQPGPKGNV-----GPGSEBPPGPGQGNPGAQ 765
QY 276 GL-GGGGGMGRREARSELGIALRG-----GAADPPCHYEKVSVDYGHVYIVODGP 329
DB 766 GLPGQGAIGP-----PGEKGPLGKPLPGMPGADGP-----GHP-----GKSGP 806
QY 330 P-----QSPPP 334
```

```
Db      807 PGEKGGQGP 816

RESULT 12
US-10-821-234-914
; Sequence 914, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; PRIOR FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 914
; LENGTH: 1532
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-821-234-914

Query Match
Best Local Similarity 23.5%; Score 135.5; DB 6; Length 1532;
Matches 69; Conservative 18; Mismatches 102; Indels 105; Gaps 11;

Qy      65 APPGPHSSPNYEFYKLYLVGGAQGR-----CEAPPANLLLTCDRPDLDLRFITKF 117
Db      684 AGEPRGHGPPG-----VPGSVGPKGSSGSPGPGPPG----- 716

Qy      118 QEYSPLWMEHRSNHDYIITATSDTRRGESLGGVCLTRGMKYLAVGSPRGAVP 177
Db      717 -----VGLQGLRGEVGLP-GVK-----GDKGPMGP 740

Qy      178 RKPVESEMERDGAHSLPEKGNLPDPTSNATSGAEGPLPPSPMPAVAGAGLAL 237
Db      741 PEPKPDQSGKRGRLTG--EPKMGRLPG-AVGEPRKAKGMAPRGHGGPRGEGQ---- 793

Qy      238 LLLGVAGAGAMCWRRRRAKPSERHPG-PGSFGRGSLGLGGGGMGPREAPGELGIA 296
Db      794 -LTGMPGI-----RGPFGSGDPGKPGLTGPGQGLPQTGPRIKGPBPAPGKI 843

Qy      297 LRGGA-----DPPCPHYEKVSGDYGHPIYIVQDPPQSP 333
Db      844 VTSEGSMLTVPGPPPGAMPBPAGAPGAPGALPQHDEVLNLQSPGPP 897

RESULT 13
US-10-821-234-1431
; Sequence 1431, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; PRIOR FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1431
; LENGTH: 1366
; TYPE: PRT
; ORGANISM: Homo sapiens
```

```
US-10-821-234-1431

Query Match
Best Local Similarity 25.3%; Score 134.5; DB 6; Length 1366;
Matches 89; Conservative 14; Mismatches 114; Indels 135; Gaps 22;

Qy      3 PPHSGPGV--RYGALLLLGLVGLSLSEVYNNANKRQAAGGYLYVQIGDRDL 60
Db      321 PGLPGRPGIPGVGAAGATGARGLVGEPPAGSKGSGKKGPPGAG-----PQ----- 369

Qy      61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGR-----CEAPPANLLLTCDRPDLDLRF 113
Db      370 -----GPPGP-----SGEKKRPNSEAGSAGFP----- 395

Qy      114 TIKQEYSPNLWMEHRSNHDYIITATSDTRRGESLGGVCLTRGMKYLAVG-QSPR 172
Db      396 -----PGLRG-----SPGSR-GLPGADG-----RAGWGP 420

Qy      173 GGAVPRKPVSEMERDGAHSLPE--GKGNLPGDPTSNATSGAEGPLPPSPMPAVA 229
Db      421 GSRGASGPAVGRPGNDAGRPG--EPGLMGPRGLGSP-GNIGPAKKEGPV---GLPGID 474

Qy      230 GAAAGLALLLGAVAGAGAMCWRRRRAKPSERHPG-----PSFGRGSLGLGGG-G 281
Db      475 GRPG-----IGPAG-----RGEPRNIGFPGPKPTGDPKNGDKHAGLAGARG 520

Qy      282 GMP-----REAPGELGIALRG---GAADP---FCPHYEKVSGDYGP 321
Db      521 AGPFGNNGAQGPFGPGV--QCGKGEGQAPGPFPGQLFGSPGAGVGP 570

RESULT 14
US-11-186-284-31
; Sequence 31, Application US/11186284
; Publication No. US2005026493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamackar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MPW01-029P2RNM
; CURRENT APPLICATION NUMBER: US/11/186,284
; PRIOR FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 1366
; TYPE: PRT
; ORGANISM: Homo Sapiens

US-11-186-284-31

Query Match
Best Local Similarity 25.3%; Score 134.5; DB 7; Length 1366;
Matches 89; Conservative 14; Mismatches 114; Indels 135; Gaps 22;

Qy      3 PPHSGPGV--RYGALLLLGLVGLSLSEVYNNANKRQAAGGYLYVQIGDRDL 60
Db      321 PGLPGRPGIPGVGAAGATGARGLVGEPPAGSKGSGKKGPPGAG-----PQ----- 369
```


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GenCore version 5.1.6
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OW protein - protein search, using sw model

Run on: December 21, 2005, 14:22:09 / Search time 28.044 Seconds
(without alignments)

1561.068 Million cell updates/sec

Title: US-10-021-121-2

Perfect score: 2450
Sequence: 1 MCPPHSGPGVRVAGALLIG.....TTLLRQASVEAAGQHGPL 455

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	628.5	25.7	336	2	149766	hepatoma transmembr
2	623	25.4	346	2	S46993	elk ligand - human
3	620.5	25.3	333	2	184743	hepatoma transmembr
4	604.5	24.7	345	2	148780	Strat/Bp1g2 proteob
5	599.5	24.5	345	2	158406	LEBR-2 - rat
6	214.5	8.8	237	2	T19914	hypothetical proteob
7	179	7.3	238	2	I38849	LEBR-3 - human
8	176	7.2	209	2	A54984	ELF-1 protein precu
9	175.5	7.2	213	2	JB0322	ephrin-A2 - human
10	170.5	7.0	228	2	A57084	repulsive axon gult
11	169.5	6.9	201	2	I38850	LEBR-4 - human
12	167.5	6.8	228	2	I58170	LEBR-7 precursor -
13	166	6.8	205	2	A36377	Bcl protein precu
14	159	6.5	680	2	S31216	collagen alpha 1(I(I
15	154.5	6.3	1049	1	CGBO78	collagen alpha 1(I(I
16	153.5	6.3	1670	1	CGH03B	collagen alpha 3(I(I
17	151.5	6.2	301	2	B31219	collagen 2 - Caenn
18	149	6.1	325	2	T32248	hypothetical proteob
19	149	6.1	569	2	S42886	collagen - alkwood
20	148.5	6.1	316	2	T20497	hypothetical proteob
21	148	6.0	921	2	S42617	collagen alpha 1(I(I
22	146.5	6.0	1315	2	A56101	collagen alpha 1(I(I
23	146.5	6.0	1492	2	A40333	collagen alpha 1(I(I
24	146.5	6.0	1774	2	B56101	collagen alpha 1(I(I
25	146	6.0	675	2	S20819	collagen alpha 3(I(I
26	145.5	5.9	305	2	T20906	hypothetical proteob
27	145	5.9	674	2	S13301	collagen alpha 1(I(I
28	145	5.9	931	2	S13580	collagen alpha 1(I(I
29	144.5	5.9	438	2	S53787	collagen alpha chara

30	144	5.9	1027	2	S28774	collagen alpha cha
31	143	5.8	1747	2	A54121	collagen alpha-4 c
32	142.5	5.8	635	2	A57131	collagen alpha 2(I
33	142.5	5.8	743	1	S23779	collagen alpha 1(V
34	142.5	5.8	1496	1	CGH02V	collagen alpha 2(V
35	142	5.8	614	2	T33149	hypothetical prote
36	142	5.8	744	2	S15435	collagen alpha 1(V
37	142	5.8	1029	2	S21369	collagen alpha 2(V
38	142	5.8	1763	2	S16366	collagen alpha 2(I
39	141.5	5.8	1466	1	CGH07L	collagen alpha 1(I
40	141	5.8	319	2	T32250	hypothetical prote
41	141	5.8	744	1	A34246	collagen alpha 1(V
42	141	5.8	744	1	S23298	collagen alpha 1(V
43	140.5	5.7	305	2	T30165	hypothetical prote
44	140	5.7	304	2	T22482	hypothetical prote
45	140	5.7	680	1	CGH01D	collagen alpha 1(X

ALIGNMENTS

RESULT 1
149766
hepatoma transmembrane kinase ligand - mouse
C/Species: Mus musculus (house mouse)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C/Accession: 149766
R/Bennett, B.D.; Zeigler, F.C.; Gu, O.; Fendly, B.; Goddard, A.D.; Gillett, N.; Matthews, Proc. Natl. Acad. Sci. U.S.A. 92, 1866-1870, 1995
A/Title: Molecular cloning of a ligand for the Eph-related receptor protein-tyrosine kinase
A/Accession: 149766
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-336 <RES>
A/Cross-references: UNIPROT: P52800; UNIPARC: UP1000020B55; GB: I38847; NID: g769677; PIND: ?
A/Genes: HTK

Query Match 25.7%; Score 628.5; DB 2; Length 336;

Best Local Similarity 41.8%; Pred. No. 3.2e-37; Matches 137; Conservative 49; Mismatches 129; Indels 13; Gaps 5;

QY	14	GALLIGVGLVSGSLPEPVYMNANKRFOAEGGYVLPQIGDRLDLCPRAPRPHSS	73
DB	17	GLIMVLCRTAISRISVLEPIYMNSSKFLPQGLVLYIQIGKDIICPKV---DSKTV	73
QY	74	PNYEYKLYLVGAGGRCCEAPAPNLLTCDRPDLDLFTIKQEQYSPNLGHEFRSHH	133
DB	74	GQVEYKVVYVMDQADRCCTIKKENTPLNLCARPDDVFTIKFQFSPNLGLFQKNK	133
QY	134	DYIITISGTRGLESLOGGVLTGGMKYLRLVGO--SPRGAVVRKRPVSEPMRR--DR	190
DB	134	DYIITISGTRGLESLOGGVLTGGMKYLRLVGO--SPRGAVVRKRPVSEPMRR--DR	190
QY	191	GAHSLPEKKNLPGDPTSNATSRGAEGPLRPPSPMAVGAAGLALLLVGAGAGAMC	250
DB	194	GRSSTSPYVKRPPGSGTGNKSGHSGNNLLGSEVLFAGISGCIFFIYITLVVLL	253
QY	251	WRRRAKPSRRPFGSGSLGLGGGGMGPRPAPGELGIALRGGAADPPFCFH	310
DB	254	KYRRRRKHSPOHTTLLSLTATPRKGGNN-----NGSEPSDVIIFLR---TADSVFCFH	306
QY	311	YKVSQDYGHPYIVVDGPPQSPPNITYY	338
DB	307	YKVSQDYGHPYIVVDGPPQSPPNITYY	334

RESULT 2

S46993
elk ligand - human
C/Species: Homo sapiens (man)
C/Date: 15-Jul-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004

C:Accession: S46993
R:Beckmann, M.P.; Carrecci, D.P.; Baum, P.; vanden Bos, T.; James, L.; Farrar, T.; Kozlo
EMBO J. 13, 3757-3762, 1994
A:Title: Molecular characterization of a family of ligands for eph-related tyrosine kin
A:Reference number: S46993; MIM:94349923; PMID:8070404
A:Accession: S46993
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-346 <BEC>
A:Cross-references: UNIPROT:P98172; UNIPARC:UPI000006222D; GB:U09304; NID:g538366; PIDN:
Query Match 25.4%; Score 623; DB 2; Length 346;
Best Local Similarity 39.2%; Pred. No. 8e-37;
Matches 143; Conservative 48; Mismatches 116; Indels 58; Gaps 9;
QY 8 PGGVRLGALLLLGLVGL-----SLEPYWNSANKRFOAEGGYLVLPQIGRLDLL 61
DB 4 PGGRMLGKMLVAMVVALCHLAPLAKNLEPVSWSLNPKFLSGKGLVTPKIGDKLDII 63
QY 62 CPRARPPGPHSSPNVEFYKLYLVGAQGRRCAPAPNLLTCDRPDLRLFTIKFOEYS 121
DB 64 CPRABAGRP-----YEVYKLYLVPRPOAAACSTVLDPNVLVTCNRDEQELRFTIKFOEFS 118
QY 122 PNLMGHEPSSHHDYIIATSDTRREGLESLOGGVCLTRGKVLRLVQSPRGGAIVPRKEV 181
DB 119 PNYMGLEFKKHHDYIITSNGSLBGLBNREGVCSTRTKIKIMKVGODPNVATPQLTYT 178
QY 182 SEMPMERDGAASHLE-PGKENLPDPTSNATSRGAGPLPPSPMPAVGAAGAL---- 236
DB 179 SRPSKADLVTKKATAPASRGSLGSDGKHETVNOBESGP-----GASGSSGDD 231
QY 237 -----LLLLGVAGAGA-----MCMRRRAKPSBSRHPGSGFSGSLGL 277
DB 232 GFENSKVALFAAVGAGCVFLIIIFLVTLTKLRKRRHQTQ-----RAAALSL 282
QY 278 ----GGGGMGPEARPELGLTLRGGGAADPFCHYENVSDDYGHPIYIVDGPQSP 333
DB 283 STLASPKGSGTGTGTPSDIIIFLR---TTENNYCPHYEKVSGDGHPIYIVQEMPPQSP 339
QY 334 PNIYY 338
DB 340 ANIYY 344
RESULT 3
184743
hepatoma transmembrane kinase ligand - human
C:Species: Homo sapiens (man)
C:Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 09-Jul-2004
C:Accession: 184743
R:Bennett, B.D.; Zeigler, F.C.; Gu, Q.; Fendly, B.; Goddard, A.D.; Gillett, N.; Matthews
Proc. Natl. Acad. Sci. U.S.A. 92, 1866-1870, 1995
A:Title: Molecular cloning of a ligand for the EPH-related receptor protein-tyrosine kin
A:Reference number: 149766; MIM:9519254; PMID:7534404
A:Accession: 184743
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-333 <RES>
A:Cross-references: UNIPROT:P52799; UNIPARC:UPI0000129C9B; GB:L38734; NID:g769675; PIDN:
C:Genetics:
A:Gene: GDB:EPUG5; LERK5
A:Cross-references: GDB:438338; OMIM:600527
A:Map position: 13q33-13q33
Query Match 25.3%; Score 620.5; DB 2; Length 333;
Best Local Similarity 40.5%; Pred. No. 1.1e-36;
Matches 133; Conservative 52; Mismatches 130; Indels 13; Gaps 5;
QY 14 GALLLGVILGVGLSLEPYWNSANKRFOAEGGYLVLPQIGRLDLLCPRAPPPGPHS 73
DB 14 GVLMLVCRAAISSTVLEPIYWNSSSKFLPGGLVLVLPQIGDKLIIICPKV---DSKIV 70
QY 74 PNVEFYKLYLVGAQGRRCAPAPNLLTCDRPDLRLFTIKFOEYSPNLMGHEFRSH 133

DB 71 GQVEYKLYVMVDKDAADRRTIKENTPPLNCAKPPQDIKFTIKFOEFSPNLWGLEFOKMK 130
QY 134 DVIYIATSDTRREGLESLOGGVCLTRGMKVLRLVQC--SPRGGAIVPRKPSSEMPMR-DR 190
DB 131 DVIYIATSDTRREGLESLOGGVCLTRGMKVLRLVQC--SPRGGAIVPRKPSSEMPMR-DR 190
QY 191 GAHSLPEKKNLPDPTSNATSRGAGPLPPSPMPAVGAAGLALLLVAGAGCAGMC 250
DB 191 GSSSTTSPVKPNPSSSTGNSAGSNIIIGSEVALFAGIASGCIIFVYIITVLVLL 250
QY 251 WRRRAKPEESHRRPGRSGRGSGLGCGGCMGRAREPGLIALRGGGAADPFPCPH 310
DB 251 KYRRRRRKHSPPHTTTLSLTATPRSGNN---NGSEPSDIIIFLR---TADSVCPH 303
QY 311 YEKVSGDYGHPIYIVODGPQSPNNIYY 338
DB 304 YEKVSGDYGHPIYIVQEMPPQSPANNIYY 331
RESULT 4
148780
Stral/Ep1g2 protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: 148780; A55507; A55062; S52670
R:Bouillet, P.; Oulad-Abdelghani, M.; Vicaire, S.; Garnier, J.M.; Schaubaur, B.; Dolle, P.
Dev. Biol. 170, 420-433, 1995
A:Title: Efficient cloning of cDNAs of retinoic acid-responsive genes in P19 embryonal ce
A:Reference number: 148780; MIM:95377533; PMID:7649373
A:Accession: 148780
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-345 <RES>
A:Cross-references: UNIPROT:P52795; UNIPARC:UPI0000018AC; EMBL:248781; NID:g747858; PIDN:
R:Plancher, P.A.; Renshaw, B.; Hollingsworth, T.; Baum, P.; Lyman, S.D.; Jenkins, N.A.; C
Genomics 24, 127-132, 1994
A:Title: Genomic organization and chromosomal localization of mouse Ep1g2, a gene encodin
A:Reference number: A55507; MIM:95203867; PMID:7896266
A:Accession: A55507
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-345 <FLB>
A:Cross-references: UNIPARC:UPI0000018AC; GB:U07598
R:Shao, H.; Lou, L.; Pandey, A.; Pasquale, E.B.; Dixit, V.M.
J. Biol. Chem. 269, 26606-26609, 1994
A:Title: cDNA cloning and characterization of a ligand for the Cxk5 receptor protein-tyr
A:Reference number: A55062; MIM:95014510; PMID:7929389
A:Accession: A55062
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-89; 'T', 91-345 <SHA>
A:Cross-references: UNIPARC:UPI000016CADF; GB:U12983; NID:g575928; PIDN:AAA53231.1; PID:5
C:Genetics:
A:Gene: EPUG2
Query Match 24.7%; Score 604.5; DB 2; Length 345;
Best Local Similarity 37.9%; Pred. No. 1.6e-35;
Matches 136; Conservative 51; Mismatches 107; Indels 65; Gaps 10;
QY 15 ALLLGVILGVGL--SLEPYWNSANKRFOAEGGYLVLPQIGRLDLLCPRAPPPGPHS 72
DB 15 AMVAVTLCLRLATPLAKNLEPVSWSLNPKFLSGKGLVTPKIGDKLDIIICPRAEAGRP-- 72
QY 73 SNVEFYKLYLVGAQGRRCAPAPNLLTCDRPDLRLFTIKFOEYSPNLMGHEFRSH 132
DB 73 ---YEVYKLYLVPRPOAAACSTVLDPNVLVTCNKPHQELRFTIKFOEYSPNMGLEFKKY 129
QY 133 HDYIATSDTRREGLESLOGGVCLTRGMKVLRLVQSPRGGAIVPRKPSSEMPMERDGA 192
DB 130 HDYIATSDTRREGLESLOGGVCLTRGMKVLRLVQSPRGGAIVPRKPSSEMPMERDGA 192
QY 193 AHSLEPKKNLPDPTSNATSRGAGP-----LPPSPMPAVGAAG-----LA 236

```

Db      189 VKT-----A|Q|A|P|R|G|S|Q|G|S|D|G|K|H|E|T|V|N|O|E|K|S|G|G|A|G|G|S|G|S|D|S|F|F|N|S|K| 236
Qy      237 L|L|L|L|G|V|A|G|A|G|A|-----M|C|W|R|R|R|R|A|K|P|S|E|R|H|P|G|S|F|G|S|G|L|G|-----G|G| 279
Db      237 V|A|L|F|A|V|A|G|A|G|C|V|F|L|L|I|I|F|L|V|L|L|K|R|R|R|K|H|Q|-----R|A|A|L|S|L|T|A|S|P| 287
Qy      280 G|G|G|M|G|R|E|A|P|G|E|L|A|L|R|G|G|A|D|P|P|C|P|H|Y|E|K|V|S|G|D|G|H|P|Y|I|V|O|D|G|P|G|S|P|P|N|I|Y| 338
Db      288 K|G|S|G|T|A|G|T|E|P|S|D|I|I|P|L|R|-----T|T|E|N|N|Y|C|P|H|Y|E|K|V|S|G|D|G|H|P|Y|I|V|O|E|P|P|G|S|P|A|N|I|Y| 343

RESULT 5
158406      LERK-2 - rat
C:/Species: Rattus norvegicus (Norway rat)
C:/Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C:/Accession: 158406
R:/Fletcher, F.A.; Carpenter, M.; Shilling, H.; Baum, P.; Ziegler, S.; Gimpel, S.; Hollitt
Oncogene 9, 3241-3248, 1994
A:/Title: LERK-2, a ligand for the receptor tyrosine kinase ELK, is evolutionarily conserved
A:/Reference number: 158406; MUID:95022634; PMID:7936648
A:/Accession: 158406
A:/Status: preliminary; translated from GB/EMBL/DBJ
A:/Molecule type: mRNA
A:/Residues: 1-345 <RES>
A:/Cross-references: UNIPROT:P52796; UNIPARC:UPI0000129C98; EMBL:U07560; NID:9563118; PID
C:/Genetics:
A:/Gene: Eplg2

Query Match      24.5%; Score 599.5; DB 2; Length 345;
Best Local Similarity 37.6%; Pred. No. 3.6e-35;
Matches 135; Conservative 52; Mismatches 107; Indels 65; Gaps 10;

Qy      15 A|L|L|L|G|V|L|G|V|S|L|-----S|L|E|P|V|Y|N|S|A|N|K|R|Q|A|E|G|V|L|P|Q|I|D|R|D|L|C|P|R|A|P|P|S| 72
Db      15 A|V|V|L|L|C|L|R|A|P|L|A|L|L|E|P|V|S|S|L|N|P|R|K|S|G|G|V|I|Y|P|K|I|G|D|K|D|I|I|C|P|R|A|E|A|G|R|P| 72
Qy      73 S|N|V|E|F|Y|K|L|Y|V|G|A|Q|R|C|E|A|P|A|P|N|L|L|T|C|R|P|D|L|R|F|T|I|K|F|Q|E|Y|S|P|N|L|M|G|H|E|R|S|H| 132
Db      73 ---Y|E|Y|K|L|Y|V|R|E|Q|A|A|A|C|S|T|V|D|P|N|V|T|C|N|K|P|Q|E|R|F|T|I|K|F|Q|E|S|E|N|Y|G|L|E|F|K|X| 129
Qy      133 H|D|Y|I|A|T|S|D|T|R|E|G|L|S|L|Q|G|V|C|L|T|R|G|K|V|L|R|V|Q|S|P|R|G|A|V|P|R|K|P|V|S|E|M|E|R|D|R|G|A| 192
Db      130 H|O|Y|I|T|S|T|N|G|S|L|E|G|E|N|E|G|V|C|R|T|R|K|I|K|V|K|V|Q|D|P|N|A|T|P|Q|L|T|T|S|R|S|K|S|D|W|T| 188
Qy      193 A|N|S|L|E|P|G|E|N|L|R|E|D|P|R|S|A|N|T|S|R|G|A|E|R|-----L|P|R|P|S|P|A|V|A|G|A|G|-----L|A| 236
Db      189 V|K|T|-----A|T|Q|A|P|R|G|S|Q|G|S|D|G|K|H|E|T|V|N|O|E|K|S|G|G|A|G|G|S|G|S|D|S|F|F|N|S|K| 236
Qy      237 L|L|L|L|G|V|A|G|A|G|A|-----M|C|W|R|R|R|R|A|K|P|S|E|R|H|P|G|S|F|G|S|G|L|G|-----G|G| 279
Db      237 V|A|L|F|A|V|A|G|A|G|C|V|F|L|I|I|F|L|V|L|L|K|R|R|R|K|H|Q|-----R|A|A|L|S|L|T|A|S|P| 287
Qy      280 G|G|G|M|G|R|E|A|P|G|E|L|A|L|R|G|G|A|D|P|P|C|P|H|Y|E|K|V|S|G|D|G|H|P|Y|I|V|O|D|G|P|G|S|P|P|N|I|Y| 338
Db      288 K|D|S|G|T|A|G|T|E|P|S|D|I|I|P|L|R|-----T|T|E|N|N|Y|C|P|H|Y|E|K|V|S|G|D|G|H|P|Y|I|V|O|E|P|P|G|S|P|A|N|I|Y| 343

RESULT 6
119914      hypothetical protein C43F9.8 - Caenorhabditis elegans
C:/Species: Caenorhabditis elegans
C:/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:/Accession: T19914
R:/Mortimore, B.
submitted to the EMBL Data Library, November 1996
A:/Reference number: Z19195
A:/Accession: T19914
A:/Status: preliminary; translated from GB/EMBL/DBJ
A:/Molecule type: DNA
A:/Residues: 1-237 <WIL>
A:/Cross-references: UNIPROT:Q9U3M2; UNIPARC:UPI0000078016; EMBL:Z82362; PIDD:CA854195.1;

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A:/Experimental source: clone C43F9
C:/Genetics:
A:/Gene: CESP:C43F9.8
A:/Map position: 4
A:/Introns: 32/2; 96/3; 214/1

Query Match      8.8%; Score 214.5; DB 2; Length 237;
Best Local Similarity 25.7%; Pred. No. 4e-08;
Matches 53; Conservative 41; Mismatches 83; Indels 29; Gaps 6;

Qy      11 V|R|V|G|A|L|L|G|V|L|S|-----G|L|S|E|P|V|Y|N|S|A|N|K|R|Q|A|E|G|V|L|P|Q|I|D|R|D|L|C|P|R|A|P|P| 68
Db      1 M|Q|I|A|T|L|L|S|L|P|P|I|G|M|A|R|K|I|D|I|N|I|S|N|P|I|F|D|V|S|N|T|D|H|V|S|V|H|I|G|R|V|S|I|R|C|P|S|D|E|T| 60
Qy      69 G|P|H|S|P|N|V|E|F|Y|K|L|Y|V|G|A|Q|R|C|E|A|P|A|P|N|L|L|T|C|R|P|D|L|R|F|T|I|K|F|Q|E|Y|S|P|N|L|M|G|H|E| 128
Db      61 G|-----K|Y|E|S|Y|I|Y|W|S|D|E|Y|D|H|C|F|L|S|K|R|V|L|G|A|C|D|N|G|T|I|N|A|S|I|N|I|V|R|S|F|P|T|G|G|F|E| 114
Qy      129 F|R|S|H|D|Y|I|A|-----T|S|D|T|R|E|G|L|S|L|Q|G|V|C|L|T|R|G|K|V|L|R|V|Q| 169
Db      115 F|Q|P|K|V|Y|F|L|S|K|S|E|V|D|A|L|I|Y|E|T|A|N|Q|I|P|Q|T|S|D|T|G|L|E|I|D|R|K|D|G|L|C|T|A|K|O|M|K|I|K|E|V|Q| 174
Qy      170 S|P|R|G|A|V|P|R|K|P|V|S|E|M|E|R|D|R|G|A|H|S| 195
Db      175 D|R|R|G|I|E|N|P|K|-----P|A|R|T|L|K|D|R|D|A|E|H|S| 198

RESULT 7
138849      LERK-3 - human
C:/Species: Homo sapiens (man)
C:/Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C:/Accession: I38849
R:/Kozlosky, C.J.; Marakovsky, E.; McGrew, J.T.; Vandenbos, T.; Teepe, M.; Lyman, S.D.; &
Oncogene 10, 299-306, 1995
A:/Title: Ligands for the receptor tyrosine kinases hsk and elk: isolation of cDNAs encoding
A:/Reference number: I38849; MUID:95140419; PMID:7838529
A:/Accession: I38849
A:/Status: preliminary; translated from GB/EMBL/DBJ
A:/Molecule type: mRNA
A:/Residues: 1-238 <RES>
A:/Cross-references: UNIPROT:P52797; UNIPARC:UPI0000129C9F; EMBL:U14187; NID:9642832; PIDN
C:/Genetics:
A:/Gene: GDB:EPLG3
A:/Map position: 1q21-1q22
A:/Cross-references: GDB:438336; OMIM:601381
C:/Superfamily: axon guidance signal protein

Query Match      7.3%; Score 179; DB 2; Length 238;
Best Local Similarity 28.4%; Pred. No. 1.3e-05;
Matches 65; Conservative 24; Mismatches 80; Indels 60; Gaps 12;

Qy      7 G|P|G|V|R|V|G|A|L|L|G|V|L|S|L|E|P|V|Y|N|S|A|N|K|R|Q|A|E|G|V|L|P|Q|I|D|R|D|L|C|P|-----R| 64
Db      24 G|P|G|-----G|A|L|G|-----N|R|H|A|V|Y|N|S|N|O|H|L|R|E|G|Y|V|Q|V|N|V|A|D|Y|D|I|Y|C|P|H|Y|N| 67
Qy      65 A|R|P|P|G|H|S|P|-----N|Y|E|F|Y|K|L|Y|V|G|A|Q|R|C|E|A|P|A|P|N|L|L|T|C|R|P|D|L|-----D|I|R|F|T|I|K| 117
Db      68 S|S|G|V|G|A|P|G|P|G|G|A|B|Q|V|L|Y|W|S|B|R|N|G|Y|R|T|C|N|A|S|G|E|F|K|-----R|W|E|C|N|R|P|H|A|P|S|I|K|S|E|F| 126
Qy      118 Q|E|Y|S|P|L|M|G|H|E|R|S|H|D|Y|I|A|T|S|D|T|R|E|G|L|S|L|Q|G|V|C|L|T|R|G|K|V|L|R|V|Q|S|P|R|G|A|V|P| 177
Db      127 Q|R|Y|S|A|F|S|L|G|E|F|R|H|A|G|E|Y|I|S|T|P|H|N|L|-----W|K|L|R|-----M|V|F|V|C|A|S|T|S|H|G|----- 174
Qy      178 R|K|P|V|S|E|P|-----M|E|R|D|R|G|A|H|S|L|-----P|G|K|E|N|L|P| 204
Db      175 E|K|P|V|T|L|P|Q|T|M|G|P|N|V|K|I|N|V|L|D|P|G|E|N|Q|V|P|K|L|E|K|S|I|S|T|S|P|R|K|B|H|P| 223

RESULT 8
A54984      ELF-1 protein precursor - mouse
N:/Alternate names: Cek1 ligand

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C:/Species: Mus musculus (house mouse)
C:/Date: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 09-Jul-2004
C:/Accession: A54984; A55873
R:/Cheng, H.J.; Flanagan, J.G.
Cell 79, 157-168, 1994
A:/Title: Identification and cloning of ELF-1, a developmentally expressed ligand for the
A:/Reference number: A54984; MUID:9500776; PMID:7522971
A:/Accession: A54984
A:/Status: preliminary
A:/Molecule type: mRNA
A:/Residues: 1-209 <SHA>
A:/Cross-references: UNIPROT:P52801; UNIPARC:UPI0000020CE3; GB:U14941; NID:G558836; PIDN:
R:/Shao, H.; Lou, L.; Pandey, A.; Verderame, M.F.; Stever, D.A.; Dixit, V.M.
J. Biol. Chem. 270, 3467-3470, 1995
A:/Title: cDNA cloning and characterization of a Cdk7 receptor protein-tyrosine kinase 1
A:/Reference number: A55873; MUID:95181289; PMID:7876076
A:/Accession: A55873
A:/Status: preliminary
A:/Molecule type: mRNA
A:/Residues: 1-209 <SHA>
A:/Cross-references: UNIPARC:UPI0000020CE3; GB:U14752; NID:G681886; PIDN:AAA68520.1; PID:
C:/Superfamily: axon guidance signal protein
C:/Keywords: lipoprotein; membrane protein

Query Match 7.2%; Score 176; DB 2; Length 209;
Best Local Similarity 29.3%; Pred. No. 1.8e-05;
Matches 58; Conservative 19; Mismatches 69; Indels 52; Gaps 7;

QY 33 VYVNSANKRFOAE-----GGYVLYPQIGRLDLCPRARPPGPHSSPNVEFYKLYLVGA 87
DB 35 VYVNRNRPFRQYSAVGDGGYTVESINDYLDYCHYGALP-PRMERHYLVVWNGE 93
QY 88 QGRRCAPAPNLLTCDRBDL---DLRFITKFOEYSPNLMGHEFRSHHDYIIATSDGT 144
DB 94 GHASCHDRQGRGFRMWEKNRPAACGPLKSEKQLTTPSLGEPFRGHEHYIISITP--- 151
QY 145 REGLESLOGGVCLTRGMKVLIRVGQSPRGAVPRKPVSEMPERDRGAHSLPEKKNLP 204
DB 152 ----PVLVDRPCLR--LKYVVR-----PTNBTLY 174
QY 205 GDP---TSNATSRGAG 218
DB 175 EAPEPIFTSNSSCSGLGG 192

RESULT 9
JEO322
epnrlin-A2 - human
C:/Species: Homo sapiens (man)
C:/Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 09-Jul-2004
C:/Accession: JEO322
R:/Asheim, H.; Pedetour, F.; Grosgeorge, J.; Logtenberg, T.
Biochem. Biophys. Res. Commun. 252, 378-382, 1998
A:/Title: Cloning, chromosomal mapping, and tissue expression of the gene encoding the huma
A:/Reference number: JEO322; MUID:99045414; PMID:9826538
A:/Accession: JEO322
A:/Status: preliminary
A:/Molecule type: mRNA
A:/Residues: 1-213 <NMS>
A:/Cross-references: UNIPROT:O43921; UNIPARC:UPI0000164442; GB:AJ007292; NID:G3688367; PI
C:/Superfamily: axon guidance signal protein

Query Match 7.2%; Score 175.5; DB 2; Length 213;
Best Local Similarity 36.8%; Pred. No. 2e-05;
Matches 43; Conservative 14; Mismatches 51; Indels 9; Gaps 3;

QY 33 VYVNSANKRFOA-----EGGYVLYPQIGRLDLCPRARPPGPHSSPNVEFYKLYLVGA 87
DB 39 VYVNRNRPFRHAAGDGGYTVESINDYLDYCHYGALP-PRMERHYLVVWNGE 97
QY 88 QGRRCAPAPNLLTCDRBDL---DLRFITKFOEYSPNLMGHEFRSHHDYIIATSDGT 141
DB 98 GHASCHDRQGRGFRMWEKNRPAACGPLKSEKQLTTPSLGEPFRGHEHYIISITP 154

RESULT 10
A57084
reputive axon guidance signal protein RAGS precursor - chicken
C:/Species: Gallus gallus (chicken)
C:/Date: 03-Nov-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C:/Accession: A57084
R:/Drescher, U.; Kremsner, C.; Handwerker, C.; Loeschinger, J.; Noda, M.; Bonhoeffer, F.
Cell 82, 359-370, 1995
A:/Title: In vitro guidance of retinal ganglion cell axons by RAGS, a 25 kDa tectal protei
A:/Reference number: A57084; MUID:95560980; PMID:7634326
A:/Accession: A57084
A:/Status: preliminary; not compared with conceptual translation
A:/Molecule type: mRNA
A:/Residues: 1-228 <DRS>
A:/Cross-references: UNIPROT:P52804; UNIPARC:UPI0000129C92; GB:X90377; NID:G106113; PIDN:
C:/Superfamily: axon guidance signal protein
C:/Keywords: glycoprotein; membrane protein; phosphatidylinositol linkage
F/1-20/Domain: signal sequence #status predicted <SIG>

Query Match 7.0%; Score 170.5; DB 2; Length 228;
Best Local Similarity 28.9%; Pred. No. 5e-05;
Matches 73; Conservative 30; Mismatches 91; Indels 59; Gaps 13;

QY 16 LLLIGVLGI-VSGLSLEP-----VYVNSANKRFOAEGGYVLYPQIGRLDLCPR 64
DB 6 MLLIAVAAALWCVRGQEPGRKAVADRVAVYVNSVTPRFQ-QGDYHIDVCINDYLDVFCPH 64
QY 65 ARPPGPHSSPNVEFYKLYV-----GAQGRCEAPAPNLLTCDRBDLDR 112
DB 65 YEDSVPEKDT--ERYVLVWVNFQYSSCDHISKGRMECNRPNSN-----GPKL 113
QY 113 FTIKFOEYSPNLMGHEFRSHHDYIIATSDGTREGLESLOGGVCLTRGMKVLIRVQ 169
DB 114 FSEKQLTTPSLGEPFRGHEHYIISITP-----CLK--LKVFR--- 159
QY 170 SPRGAVPRKPVSEMPERDRGAHSLPEKKNLPDPTSNATSRGAGSLPPPSMP--A 227
DB 160 -PANSCKMTIGVHDRVVDVNDKVENSLPEADDTV---RESAPSRG-ENAAQTPIRFL 214
QY 228 VAGAAGLALLL 240
DB 215 IATLFLAMLLI 227

RESULT 11
138850
LERK-4 - human
C:/Species: Homo sapiens (man)
C:/Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C:/Accession: 138850
R:/Kozlovsky, C.J.; Maraskovsky, E.; McGrew, J.T.; Vandenbos, T.; Teepe, M.; Lyman, S.D.; &
Oncogene 10, 299-306, 1995
A:/Title: Ligands for the receptor tyrosine kinases hek and elk: isolation of cDNAs encodi
A:/Reference number: 138849; MUID:95140419; PMID:7838529
A:/Accession: 138850
A:/Status: preliminary; translated from GB/EMBL/DBJ
A:/Molecule type: mRNA
A:/Residues: 1-201 <RES>
A:/Cross-references: UNIPROT:P52798; UNIPARC:UPI0000129C90; EMBL:U14188; NID:G642834; PID
C:/Genetics:
A:/Gene: GDB:EPLG4
A:/Cross-references: GDB:438337; OMIM:601380
A:/Map position: 1q21-q22
C:/Superfamily: axon guidance signal protein

Query Match 6.9%; Score 169.5; DB 2; Length 201;
Best Local Similarity 29.9%; Pred. No. 5.1e-05;
Matches 66; Conservative 18; Mismatches 82; Indels 55; Gaps 10;

QY 24 LVSGLSL-EPVYVNSANKRFOAEGGYVLYPQIGRLDLCPRARPPGPHSSPNVEFYKLY 82

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Db      20  LRGGSLRHVVYWMNSNRLLLRGDVVELGLNDYLDICPHYEGRGPEGP--EYFALY 76
Qy      83  LVGAQGRCEAP-PAPNLLLTCDRPDLDLRTTFQESPNLMGHEPRSHDDYTIATS 141
        :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      77  MVDMPGESCOAEGRAYRWCSLPFGHVGSFKIQFTPSLGFEEFLGTEYYIISVP 136
Qy      142 DGTREGESLGGGVLTIRGMKVLRLVGGSPRGCAVPRKRVSEMPMERDRGAHSLPEGR 201
        :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      137 --TPE-----SSGQCL-----RLQVSYCKEKRESSESHPV----- 164
Qy      202 NLPGDPTSNATS--RGAEGLPPPSMPAVAGAAAGLALLL 240
        :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      165 --GSPGESGTSGMRGSDTPSP-----LCULL 189
        :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

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RESULT 12
158170
LEK-7 Precursor - human
N/Alternate names: AL-1
C/Species: Homo sapiens (man)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C/Accession: 158170, G01812
R/Winslow, J.W.; Moran, P.; Valverde, J.; Shih, A.; Yuan, J.Q.; Wong, S.C.; Tsai, S.P.;
Neuron 14, 973-981, 1995
A>Title: Cloning of AL-1, a ligand for an Eph-related tyrosine kinase receptor involved
A/Reference number: 158170, PMID:95267434, PMID:7748564
A/Accession: 158170
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residue: 1-228 <RES>
A/Cross-references: UNIPROT:P52803, UNIPARC:UPI0000129693; GB:S77167; NID:G914184; PID:G
R/Kozlosky, C.J.; Vandenhoef, T.; Park, L.S.; Cerretti, D.P.; Carpenter, M.K.
Submitted to the EMBL Data Library, May 1995

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A;Accession: G01812
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-228 <KOZ>
A;Cross-references: UNIPARC:UPI0000129C93, EMBL:U26403, NID:g1019430, PTDN:AA60377.1, P
C;GeneCDS:
A;Gene: GDB:EPLG7, AFI, LERK7
A;Cross-references: GDB:568757, OMIM:601535
A;Map position: 13q33-13q33
A;Superfamily: axon guidance signal protein

	Query Match	6.8%	Score 167.5	DB 2	Length 228		
	Best Local Similarity	28.8%	Pred. No. 8.1e-05				
	Matches	65	Conservative	29	Mismatches	81	
				Indels	51	Gaps	11
<hr/>							
QY	33	VYVNSANKRFQAEAGYLVPQIGRLDLCPPARPFGHSSPNVEFYLYLVG-----	85				
Db	34	VYVNSSNPFRG-RDDYHIDVICINDYLDVCFCHYEDESDPEDKT--ERYLLYWNEDGYGAC	90				
QY	86	-----GAGGRCEAPPAANILLTCDRPLDRFTIKPQEYSPNLMGHGFRRSHDYIAT	140				
Db	91	DHTSKGFGEWECNRPHSPN-----GPLTFSEKPOLFTFSGEGFFRGRETYISS	141				
QY	141	S---DGTREGLESLOGVCILTRGMKVLRVGQSPEKGAVPPKPVSSEMERMEDRGAAHSLE	197				
Db	142	AIPDNGBARS-----CLK--LKVFR-----PTNSCMKITGVHDVDFVDNDKYENGLE	186				
QY	198	PGKNLTPODPPTSNTSRGAEGRLPPPSPAYAAGAALALLLGVA	243				
Db	187	PADTV--HESAEPSPRG-ENNAQTPIRSRL-----LATILLFLLA	223				

RESULT 13
A36377
B61 protein precursor - human
C1Species: Homo sapiens (man)
C1Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 09-Jul-2004
C1Accession: A36377
C1Holzman, L.B.; Marks, R.M.; Dixit, V.M.

Mol. Cell. Bio. 10, 5830-5838, 1990
A;Title: A novel immediate-early response gene of endothelium is induced by cytokines and
A;Reference number: A36377; MUID:91042512, PMID:2233719
A;Accession: A36377
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-205 <HOL>
A;Cross-references: UNIPROT:P20827, UNIPARC:UPI0000129C89; GB:M57730; GB:M37476; NID:G175
C;Superfamily: axon guidance signal protein

Query Match	6.8%	Score 166	DB 2	Length 205
Best Local Similarity	27.5%	Pred. No. 9.2e-05		
Matches 46	Conservative 31	Mismatches 74	Indels 16	Gaps 5

QY 18 LLGLVGLVSGSLSEVYNNANKRRQAAGGYLYQIIGRDLCLPPRAPPGHSPN-- 75
 QY 18 LLGLVGLVSGSLSEVYNNANKRRQAAGGYLYQIIGRDLCLPPRAPPGHSPN-- 75
 Db 8 LLGLCCSLAADRLHTVFNNSSNPKEFRNE-DYTIHQVQLNDYVDIICPHYH---DHSVADAA 63
 QY 76 YEFKLYLVGGAOGRCEAPAPAPNLLTCDRDL---DLRFITKOEYEPNLMGFHFRSH 132
 Db 64 MEQITILVYHEHRYQLCCPQSKDQYRMQCNRRSAGHGPEKLSSEKQRFPTFLGKEFKG 123
 QY 133 HDYITIANSDGTRGSLSLQGGVCLITRGMKVLLRVGQSPRGGAIVPRK 179
 Db 124 HSYIYISKPIHQHEDR-----CLRLKVTYSGKTIISQAVHNNDQ 163

RESULT 14
S31216
collagen alpha 1(X) chain precursor - mouse
C/Species: Mus musculus (house mouse)
C/Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #ext change 09-Jul-2004
Accession: S31216; S28807; S22215; S30127; I48229; S26397; S31830
R/Kong, R.Y.C.; Kwan, K.M.; Lau, E.T.; Thomas, J.T.; Booc-Handford, R.P.; Grant, M.E.; CH
Eur. J. Biochem. 213, 99-111, 1993
A/Title: Intron-exon structure, alternative use of promoter and expression of the mouse c
/Reference number: S31216; MUID:93c38750; PMID:8477738

A:Accession: S31216
A:Molecule type: DNA
A:Residues: 1-680 <Kon>
A:Cross-references: UNIPROT:O05306; UNIPARC:UP1000016CBAA; EMBL:Z22610; NID:549793; PIDN
R:Elma, K., Berola, I., Rosati, R., Metsaeranta, M., Garofalo, S., Peraeae, M., de Cromo, S.
Biochem. J. 289, 247-253, 1993
A:Title: The mouse collagen X gene: complete nucleotide sequence, exon structure and expression
A:Reference number: S28807; NID:93343676; PMID:8424763

A:/Accession: S28807
A:/Molecule type: DNA
A:/Residues: 1-285, 'A', 287-680 <E1>
A:/Cross-references: UNIPARC:UPI0000026913, EMBL:X67348, NID:g50480, PINN:CAA47763.1, PID
R:/Elms: K.; Metsaers, M.; Kallio, J.; Peraelae, M.; Eerola, I.; Garofalo, S.; de Cromafalo, S.; de Cromafalo,
B. Blochm. Biophys. Acta 1130, 78-80, 1992
A:/Title: Specific hybridization probes for mouse alpha-2(Ix) and alpha-1(Ix) collagen mRNA
A:/Reference number: S22215; MUID:92182017; PMID:1543751
A:/Accession: S22215
A:/Status: preliminary
A:/Molecule type: mRNA
A:/Residues: 385-450, 'K', 452-627 <E1A>
A:/Cross-references: UNIPARC:UPI000016CBAB, EMBL:X63013, NID:g49795, PINN:CAA47741.1, PID
R:/Apte, S.S.; Olsen, B.R.
Matrix 13, 165-179, 1993
A:/Title: Characterization of the mouse type X collagen gene.
A:/Reference number: S22215; MUID:92182017; PMID:1543751

A:Reference: 530127; PMID:93261348; PMID:8492743
A:Accession: S30127
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-12, 'F', 14-26, 'S', 28-247, 'L', 249-285, 'A', 287-305, 'F', 307-416, 'S', 418-499, 'L', 501-512
A:Cross-references: UNIPARC:UPI00001773B5
R:Ape, S.S.; Seldin, M.F.; Hayashi, M.; Olsen, B.R.
Eur. J. Biochem. 206, 217-224, 1992
A:Title: Cloning of the human and mouse type X collagen genes and mapping of the mouse tyrosine phosphorylation sites
A:Accession: 148299
A:Reference: 148299; PMID:92267014; PMID:1587271
A:Accession: 148299
A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
 A:Residues: 52-247, 'L', 249-285, 'A', 287-305, 'F', 307-416, 'S', 418-499, 'L', 501-566, 'C', 568, 'A'.
 A:Cross-references: UNIPARC:UPI000016CCAC; EMBL:X65121; NID:G50482; PIDN:CAA46237.1; PID R.Summers, T.A.; Irwin, M.H.; Mayne, R.; Balian, G.
 U.Biol. Chem. 263, 581-587, 1988
 A:Title: Monoclonal antibodies to type X collagen. Bioynthetic studies using an antipep
 A:Reference number: S26397; PMID:88087150; PMID:2826450
 A:Accession: S26397
 A:Molecule type: protein
 A:Residues: 'SDGFSQ', 24-26, 'KO', <SUN>
 A:Cross-references: UNIPARC:UPI00001773B6
 C:Genetics:
 A:Gene: Col10a-1
 A:Map position: 10
 A:Insertions: 51/3
 C:Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homology
 C:Keyword: coiled coil; extracellular matrix; glycoprotein; homotrimer
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 DB 211 IGPP--GPGVGRRGNGPFGPGI-----KQDRGPGBMG----- 244
 QY 60 LCCRRARPPGSHSPYVEFYKYLVGAGGRCRCEAPPAENLITCRPDIDLFTTKFQE 119
 DB 245 ---PGPPGPGP-----GKQGR--EGIGKPAIISPPQPGI----- 277
 QY 120 YSPNLMGHERSHDYIATSDGT---REGLESQGGCLFRGMKVLRLVQSPRGA 175
 DB 278 --PGEKHPGSPG---IAGPPGAPGFGKGLPLRG---QKG-----PAG-- 314
 QY 176 VRRKPYSEMPMERDRGAHSLBPKENLPDPTSNATSRGAEPLPPSPMAVAGAAGL 235
 DB 315 LGAPGA---KGERPAG--HGDEPLRPSF---GNMGPGPKGIPGNHGIPGAKEI 364
 QY 236 ALLILGAGAGMCMRRRAKP---SESRHPC-----PGEFRGSGSLGCGGG 282
 DB 365 G--LVGPAPGPGA---RGARGPGLDGKTYGPGEPLGKNPGIPGQKDPGVGTG 419
 QY 283 M-----GPREAPGELGILRGGAADPPFCHEKVEKSGDYHAPY 323
 DB 420 LGGPVGPVAGKVPGHNGEAGPR-GEPLPTGR---GPTGPVGPFGPSKGPANP-- 472
 QY 324 IVODGP-----PQSPG 334
 DB 473 -GAPGAGIATKGLNPTGPP 492
 RESULT 15
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 C:Species: Bos primigenius taurus (cattle)
 C:Date: 04-Dec-1986 #sequence, revision 04-Dec-1986 #text change 09-Jul-2004
 C:Accession: A02862; A38001; A38002; A38003; A38004; A38005; S71946
 R:Piezsek, P.P.; Allmann, H.; Rauterberg, J.; Henkel, W.; Wachter, E.; Kuehn, K.
 Hoppe-Seyler's Z. Physiol. Chem. 360, 809-820, 1979
 A:Title: The covalent structure of calf skin type III collagen. I. The amino acid sequen
 A:Reference number: A02862; PMID:80026026; PMID:488906
 A:Accession: A02862
 A:Molecule type: protein
 A:Residues: 1-242 <PIE>
 A:Cross-references: UNIPROT:PO4258; UNIPARC:UPI0000173B8A
 R:Dewes, H.; Fietzek, P.P.; Kuehn, K.
 Hoppe-Seyler's Z. Physiol. Chem. 360, 821-832, 1979
 A:Title: The covalent structure of calf skin type III collagen. II. The amino acid sequen
 A:Reference number: A38001; PMID:80026027; PMID:488907
 A:Accession: A38001

A:Molecule type: protein
 A:Residues: 243-422 <DEW1>
 A:Cross-references: UNIPARC:UPI0000173B8B
 R:Bentz, H.; Fietzek, P.P.; Kuehn, K.
 Hoppe-Seyler's Z. Physiol. Chem. 360, 833-840, 1979
 A:Title: The covalent structure of calf skin type III collagen. III. The amino acid sequen
 A:Reference number: A38002; PMID:80026028; PMID:488908
 A:Accession: A38002
 A:Molecule type: protein
 A:Residues: 423-571 <BEN>
 A:Cross-references: UNIPARC:UPI0000173B8C
 R:Lang, H.; Glanville, R.W.; Fietzek, P.P.; Kuehn, K.
 Hoppe-Seyler's Z. Physiol. Chem. 360, 841-850, 1979
 A:Title: The covalent structure of calf skin type III collagen. IV. The amino acid sequen
 A:Reference number: A38003; PMID:80026029; PMID:488909
 A:Accession: A38003
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 A:Cross-references: UNIPARC:UPI0000173B8D
 R:Dewes, H.; Fietzek, P.P.; Kuehn, K.
 Hoppe-Seyler's Z. Physiol. Chem. 360, 851-860, 1979
 A:Title: The covalent structure of calf skin type III collagen. V. The amino acid sequen
 A:Reference number: A38004; PMID:80026030; PMID:488910
 A:Accession: A38004
 A:Molecule type: protein
 A:Residues: 809-947 <DEW2>
 A:Cross-references: UNIPARC:UPI0000173B8E
 R:Allmann, H.; Fietzek, P.P.; Glanville, R.W.; Kuehn, K.
 Hoppe-Seyler's Z. Physiol. Chem. 360, 861-868, 1979
 A:Title: The covalent structure of calf skin type III collagen. VI. The amino acid sequen
 A:Reference number: A38005; PMID:80026031; PMID:488911
 A:Accession: A38005
 A:Molecule type: protein
 A:Residues: 948-1049 <ALL>
 A:Cross-references: UNIPARC:UPI0000173B8F
 A:Experimental source: skin
 R:Henkel, W.
 Biochem. J. 318, 497-503, 1996
 A:Title: Cross-link analysis of the C-telopeptide domain from type III collagen.
 A:Reference number: S71946; PMID:8809038
 A:Accession: S71946
 A:Molecule type: protein
 A:Residues: 87-106, 107-1029, 1037-1049 <HEN>
 A:Cross-references: UNIPARC:UPI0000173B90; UNIPARC:UPI0000173B91; UNIPARC:UPI0000173B92
 C:Comment: Prolines at the third position of the tripeptide repeating unit (G-X-Y) are by
 C:Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology;
 C:Keyword: coiled coil; extracellular matrix; glycoprotein; hydroxylysine; hydroxyprolin
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 F:15-1040/Region: helical
 F:15-1040/Region: helical
 F:587-589/Region: cell attachment (R-G-D) motif
 F:752-754/Region: cell attachment (R-G-D) motif
 F:875-877/Region: cell attachment (R-G-D) motif
 F:878-880/Region: cell attachment (R-G-D) motif
 F:935-937/Region: cell attachment (R-G-D) motif
 F:1041-1049/Region: carboxyl-terminal nonhelical telopeptide
 F:95-107, 119, 938, 950/Modified site: 5-hydroxylysine (lys) #status experimental
 F:107, 950/Modified site: lysine (lys) #status predicted
 F:107/Binding site: carbonyl (lys) (covalent) #status experimental
 F:1040, 1041/Disulfide bonds: interchain #status predicted
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 DB 688 PGGSGPAPPGPGVKGGRGSPGPGAAGFCGRGPPGPGSNGNPGPGSSGAGKGG 747
 QY 203 LGDPPTSNAT-----SRGAGPLPPSPMAVAGAAGLALLGLGAGA 245
 DB 748 PPGPSNAGPSPGIGSPKDGSGPGEKGAEPGPAGPLG--LITAGRL 802

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DB      803  AGPPGMFGARGSPPGPGIKGNGKFPBSCGNGERGPFGQLPGLACTAGBPGRDGNPGS 862
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QY      293  LGIALRG-----GAADPPPCPHYEKVSGDYGHFVYIVDDGP 330
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DB      863  DGLRGRDGAFGAKGDRGENSGFAP-----GAPGHP-----GPP 896
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